

VERSION	I25259.1	GI:416368
KEYWORDS	CTLA4 counter-receptor.	
SOURCE	Homo sapiens cDNA for mRNA.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 1112)	
AUTHORS	Freeman-G-I-T-Gibben,J.G., Bousfiotis,V.A., Ng,J.W., Restivo,V.A., J., Lombard,L.A., Gray,G.S. and Nadler,L.M.	
TITLE	Cloning of B7-2, a CTLA-4 counter-receptor that costimulates human T cell proliferation (see comments).	
JOURNAL	Science 262 (5135), 909-911 (1993)	
FEATURES	94053735	
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Best Local Similarity	100.0%; Pred. No.1.5e-284;	
Matches 1112:	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Dd	1 CACAGGGTGAAGACTTTCTCTGTGCTGCTGTACAGAGGACTATGACAGACACAGCAT 60	
Oy	61 GAGTGGGTCATTCCACATATTAGTGACAGCACAGCAAGCAGCCAAAATGATGCCAGTG 120	
Dd	61 GAGTGGGTCATTCCACATATTAGTGACAGCACAGCAAGCAGCCAAAATGATGCCAGTG 120	
Oy	121 CACTATGGAGCTGAGTAACATCTCTTTTGATAGGCCTTCGTCCTCGTGTGCTGCTCC 180	
Dd	121 CACTATGGAGCTGAGTAACATCTCTTTTGATAGGCCTTCGTCCTCGTGTGCTGCTCC 180	
Oy	181 TCTGAGAGTTCAAGCTTATTTCATGAGACTSCAGACTGCGCATGCCAATTTGGCAAATC 240	
Dd	181 TCTGAGAGTTCAAGCTTATTTCATGAGACTSCAGACTGCGCATGCCAATTTGGCAAATC 240	
Oy	241 TCAAAAACAACCCGAGAGGAGCTGTAGTATTTTGGCAGGACCAGGAACCTGGTGT 300	
Dd	241 TCAAAAACAACCCGAGAGGAGCTGTAGTATTTTGGCAGGACCAGGAACCTGGTGT 300	
Oy	301 GAATGAGTATCTATAGGCAAGAGAAATTTGACAGTGTTCATTCACAGTATATGGCGG 360	
Dd	301 GAATGAGTATCTATAGGCAAGAGAAATTTGACAGTGTTCATTCACAGTATATGGCGG 360	
Oy	361 CACAAATTTTGATTTGGAGACATTTGGACCTGAGACTTCACAAATCTTCAATCAAGACAA 420	
Dd	361 CACAAATTTTGATTTGGAGACATTTGGACCTGAGACTTCACAAATCTTCAATCAAGACAA 420	

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Db	421	GGGGTTTATTAATAAGTGATCATCACACAAAAAGCCCAAGGAATGATTGCATCCACCA	480
OY	481	GATGAATTCCTGAAGTGTACAGTGGCTGTAACTTCAGTCAACTGAATAGTAGCAATTTTC	540
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Db	601	ACCTAAGAAGTGTAGTGTGTTTGGTAAAGAACCAAGCAATTCACCTATTCAGATGTGAT	660
OY	661	TATCGAGAAATCTCAGATTAATGTACAGAACTGTACAGCTTTTCATCAGCTGTCTGT	720
Db	661	TATCGAGAAATCTCAGATTAATGTACAGAACTGTACAGCTTTTCATCAGCTGTCTGT	720
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Db	721	TTTCATTCCTCATATGTACAGCAATATGACCATTCTTCTGTATTTCTGGAAACTGCACAGAC	780
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Db	1021	AAGATCTGATGAAGCCACGCTGTTTTTAAAAAGTTGCAAGACATCTTATGCGACAAAAG	1080
OY	1081	TGATACATGTTTTTAAATTAAGATGAAGGCC	1112
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RESULT	3		
LOCUS	HSU04343	1424 bp mRNA PRI	15-JUL-1996
DEFINITION	Human CD86 antigen mRNA, complete cds.		
ACCESSION	U04343		
VERSION	U04343.1 GI:439838		
KEYWORDS	B70; B7-2.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
TITLE	Azuma,M., Ito,D., Yagita,H., Okumura,K., Phillips,J.H., Lanier,L.L.		
JOURNAL	and Somoza,C.		
MEDLINE	Nature 366 (6450), 76-79 (1993)		
REFERENCE	B70 antigen is a second ligand for CTLA-4 and CD28		
AUTHORS	2 (bases 1 to 1424)		
TITLE	Fernandez-Ruiz,E., Somoza,C., Sanchez-Madrid,E. and Lanier,L.L.		
JOURNAL	CD28/CTLA-4 ligands: the gene encoding CD86 B(B70/B7.2) maps to the		
REFERENCE	same region as CD80 (B7/B7.1) gene in human chromosome 3q13-q23		
	Unpublished		
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RESULT 7
AF157827 1138 bp mRNA MAM 08-MAY-2000
LOCUS AF157827 1138 bp mRNA, complete cds.
DEFINITION Fells catus CD86 antigen (CD86) mRNA, complete cds.
ACCESSION AF157827
VERSION AF157827.1 GI:5381423
KEYWORDS
cat.
SOURCE Fells catus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 (bases 1 to 1138)
AUTHORS Choi,I.-S., Hash,S.M., Winslow,B.J. and Collisson,E.W.
TITLE Sequence analyses of feline B7 costimulatory molecules
JOURNAL Vet. Immunol. Immunopathol. 73 (3-4), 219-231 (2000)
MEDLINE 20180222
REFERENCE
2 (bases 1 to 1138)
AUTHORS Choi,I.-S., Hash,S., Winslow,B.J. and Collisson,E.W.
TITLE Direct Submission
JOURNAL Submitted (10-JUN-1999) Veterinary Pathobiology, Texas A&M University, Bldg. 1197 Rm. 222, College Station, TX 77843, USA

FEATURES
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Best local similarity 75.4%; Pred. No. 2.3e-131;
Matches 736; Conservative 0; Mismatches 222; Indels 18; Gaps 5;
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OY	161	CT	GTCTCTGTGCTGCTCCTCCTGTGAAGATTAACCTTATTTCAATGAGACGTACAGCCG	220
Db	61	CT	GTCTCTATGTGCTGCTCTTCCATGAAGAGTTCACAGATATTTTCCAAACAGACTGAGACTG	120
OY	221	CC	ATGCCAATTGGTCAAACTCTCAAAACCAAGCTGAGTACGTAGTATTTGGCAG	280
Db	121	CC	ATGCCATTTTCAAAATTTCTCAAAACATTAAGCCCTGATGATGTGTAGTGTGGGAG	180
OY	281	GACC	AGAAAACCTGGTCTGTAATAGGTATACCTTAGCAGAAAGAAATTTGACAGTGT	340
Db	181	GACC	AGGATTAAGCTGTTCTGTACACAGCTATACAGAGGCAAAAGAACCTCAAAATGTT	240
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Db	241	CATG	CAAGATATATGAGGCGCACAAAGCTTTTACAAACAACTTGGACCCCTGAGACTCAT	300
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Db	301	AAT	TTTCAATCAAGGACAAAGGCGTGTATCATATGTATCATATGTTTGGTATATATTAAGGCCCA	360
OY	461	GGA	TGATTCGCATCCACAGATGATTTCTGACAGTGCAGTGGCTTGGTAACTTCACTCA	520
Db	361	GGA	TGATTCGCATCCACAGATGATTTCTGACATATCACTGCTTCTTAACTTCACTCA	420
OY	521	CC	GAATATAGTCCATTTCTATATTAACAAAAA---TGTGATCACTAAATTTGACCTGC	577
Db	421	CC	GAATATAGTCCATTTCTATATGAACAAAAAATTTGCGACTCACTAAATTTGACCTGC	480
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Db	481	TC	ATCATATACACGGTATCCAGAACCTTAAGAAAGATGAGTGTTTGGTAAAGAACCAAGAT	540
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Db	541	TC	AAATATGAGATATATGATATATATGAGAAATCTCAATATATGTCACACAACTATAC	600
OY	698	GAG	CTTCCATCACTGCTGTCTGTTTCACTTCCCTATGTTACGAGCAATATGACCAATCTTC	757
Db	601	AAG	CTTCCATCACTGCTGTCTGTTTCACTTCCCTATGTTACGAGCAATATGACCAATCTTC	657
OY	758	TG	ATATCTGGAACATGACAAGACGGGGCTTTATATCTTCACCTTCTCTATATA	810
Db	658	TG	ATATCTGGAACATGAGTCAATGAAGTGGTCCCTCTACCTATATATATATA	710

RESULT	9
AF065897	
LOCUS	984 bp mRNA ROD
DEFINITION	Mus musculus strain A/J CD8 antigen (Cd86) mRNA, complete cds.
ACCESSION	AF065897
VERSION	AF065897.1 GI:4587839
KEYWORDS	.
SOURCE	house mouse.

	Best Local Similarity	68.4%	Pred No. 1.6e-97	
	Matches	581	Conservative	0
			Mismatches	263
			Indels	6
			Gaps	1
QY	93	CAGAAGCACCMAATGATGCCAGTGCACATAGGAGTGAATACATCTCTTTGTGA	152	
Ddb	19	CGGAAGCACCCAGATGAGACCCAGATGCACATAGGCGTTGGCAATCTATCTTTGTGA	78	
QY	153	TGGCTTCTCTGCTCTGTGGTGTGCTCTCTTGAAAGATTCAAGCTTATTCAATGACCTG	212	
Ddb	79	CAGTCTTGCTGATCTCAATGCTCTTTTCCGTGGAGACGCAAGCTTATTTCATGGGACT	138	
QY	213	CAGACCTGCATGCCAATTGTGAACCTCAAAACCAAGCCATGAGAGCTAGTAGTAT	272	
Ddb	139	CATATCTGCCGCGCCATTTCACAAAGGCTCAAAACATAGAGCTAGAGAGCTGTAGTAT	198	
QY	273	TTTTGGAGGACCAAGGAAACTGTTCGAATGAGATTTACTTTAGGCAAAAGAAATTTG	332	
Ddb	199	TTTTGGAGGACCAAGGAAAGTTGGTTCTGTAGAGACACTATTTTGGCCACAGAAACTGTG	258	
QY	333	ACAGTGTTCATCCAAAGTATATGAGCCGACACAAGTTTTGATTGGACAGTGTGAACCTTGA	392	
Ddb	259	ATAGTGTGAATGCCAAGTACCTGGGCGGACAGACTTTGACAGGAAACAATGGAGCTTAC	318	
QY	393	GACTTCACATCTTCAGATCAAGACAAAGGCTTGTATCATGTATCATTCATCAACAAA	452	
Ddb	319	GACTTCACATGTTCAGATCAAGACAAAGGCTCTATGATGTGTTTATACAAAAAAGC	378	

LOCUS	570108	1115 bp	ROD	26-JUL-2000
DEFINITION	early T cell costimulatory molecule-1		[mice, 5C2 B lymphoma cells	
ACCESSION	570108			
VERSION	570108.1	GI:546694		
KEYWORDS				
SOURCE	Mus sp.			

Db	Accession	Source	Organism	Location/Qualifiers
Db	265	TTTGGCAGGACCGCAAAAGTTGGTTCTCTGTACGACACTATTGGGACAGAAACTTGG	Mus musculus	1183 bp mRNA
Qy	333	ACAGTGTTCATTCAGATATATATGGGCGCCAGCAAGTTGATTCGGACGTTGGACCTTGA	Mus musculus	20-OCT-1995
Db	325	ATAGGTGATGATGCAGAGTACGTGGCCGACAGAGCTTTGACAGGAAACAGCTGACTTAC	Mus musculus	
Qy	393	GACTTCACATCTCTTCAGATCAACAGGAGCGGCTGTATCATGTATATCATTCACACAAA	Mus musculus	
Db	385	GACTTCACATCTCTTCAGATCAACAGGAGCGGCTGTATCATGTATATCATTCACACAAA	Mus musculus	
Qy	453	AGCCACAGAGATATATTCGATCCATCCACAGATGAAATTCGAACCTGCACTGCTTGA	Mus musculus	
Db	445	CACCCACAGAGATATATTCGATCCATCCACAGATGAAATTCGAACCTGCACTGCTTGA	Mus musculus	
Qy	513	TCACTCACTGATGATATGATACCAATTTCTATATATACGAAATATGTACATTAATTTGA	Mus musculus	
Db	505	TCACTCACTGATGATATGATACCAATTTCTATATATACGAAATATGTACATTAATTTGA	Mus musculus	
Qy	573	CCGCTCATCTATACACAGGTTACCCGAGACCTAAGAAATGATAGTTTGGCTAAGAACCA	Mus musculus	
Db	565	CCGCTCATCTATACACAGGTTACCCGAGACCTAAGAAATGATAGTTTGGCTAAGAACCA	Mus musculus	
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Db	619	CTAATATACATATGATATGATATGATATATATATATATATATATATATATATATAT	Mus musculus	
Qy	693	TGTACAGAGTTTCCATACAGCTTGTCTGTTTCATTCCTCGATGTTTCAGCAATATGACA	Mus musculus	
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Qy	753	TCTTCTGATATCTGGAATCTGACAGAGCGGCTTTTATATCTTACCTTCTCTATACAGC	Mus musculus	
Db	739	TGTGTGTGTTCTGGAATCTGACAGAGCGGCTTTTATATCTTACCTTCTCTATACAGC	Mus musculus	
Qy	813	TTGAGAGACCTTCACAGCTTGTCTGTTTCATTCCTCGATGTTTCAGCAATATGACA	Mus musculus	
Db	799	AAGGATTTTCATCTCTGGAATCTGACAGAGCGGCTTTTATATCTTACCTTCTCTATACAGC	Mus musculus	
Qy	873	TTATATATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT	Mus musculus	
Db	859	TCTCTCTGATATCTGGAATCTGACAGAGCGGCTTTTATATCTTACCTTCTCTATACAGC	Mus musculus	
Qy	933	CTCCGCACTC 942	Mus musculus	
Db	919	CCAGCAACAC 928	Mus musculus	
RESULT	15			
LOCUS	MUSB72X	1183 bp	mRNA	20-OCT-1995
DEFINITION	Murine B7-2 mRNA, complete cds.			
ACCESSION	L25606			
VERSION	L25606.1			
KEYWORDS	GI:432478			
SOURCE	Mus musculus cDNA to mRNA.			
ORGANISM	Mus musculus			
REFERENCE	Freeman, G.J., Borriello, F., Hodes, R.J., Reiser, H., Gribben, J.G., Ng, J.W., Kim, J., Goldberg, J.M., Halbrook, K., Laszlo, G., Lombard, L.A., Wang, S., Gray, G.S., Nadler, L.M., and Sharpe, A.H. Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell proliferation and interleukin 2 production J. Exp. Med. 178 (6), 2185-2192 (1993)			
AUTHORS	JOURNAL	MEDLINE	FEATURES	
	source			

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BASE COUNT	378 a 261 c 257 g 287 t
ORIGIN	

Query Match	Similarity	Score	407.2	DB	88	Length	1183
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145	CAGCTTCTGTCAT	CTCGATGCTGTTTCCGTGGAGACCGCAAGCTTATTTCAATGGAGCTG	204				
213	CAGAGCTGCATCC	CAATTTTGGCAACTCTCAAAACCAACCAAGCTGAGCTAGTAGTAT	272				
205	CATATCTGCCGTG	CCCATTTTACAAAGCTCAAAACATTAACCTCGATGAGCTGTAGTAT	264				
273	TTTGGCAGACAC	GAGAAACCTGTTCTGATAGTATACCTTAGCAAAAGCAAAATTTG	332				
265	TTTGGCAGACAC	GAGAAACCTGTTCTGATAGTATACCTTAGCAAAAGCAAAATTTG	334				
333	ACAGTGTTCAT	TCCAGTATATGGGCGCAGCAAGTTTGAATGGAGAGTTGGACCTG	392				
325	ATAGTGTGAATG	CGCAAGTACTGGGCGCAGAGCTTTGACAGAGAACACTGAGCTTAC	384				
393	GACTTTCATCT	CTTCAGATCAAGAGGCTTGTATCATCTATCATCATCAACAAA	452				
385	GACTTTCATCT	CTTCAGATCAAGAGGCTTGTATCATCTATCATCATCAACAAA	444				
453	AGCCACAGAG	AATGATTCGCATCCACAGATGAATTTGAACTGTGAGTCTGCTACT	512				
445	CACCCACAGAT	CATATTCCTCCACAGCATTTAACAGAACTGTGATGCTGACCACT	504				
513	TGAGTCAAGCT	GAAATGATGCTATATATTAACAGAAATGTGTACTAATTAATTTGA	572				
505	TGAGTCAAGCT	GAAATGATGCTATATATTAACAGAAATGTGTACTAATTAATTTGA	564				
573	CTGCTATCTAT	ATACACGGTTTACCAGAACCTAAGAAAGATGAGTGTGCTAAGAACCA	632				
565	CTGCTATCTAT	ATACACGGTTTACCAGAACCTAAGAAAGATGAGTGTGCTAAGAACCA	618				
633	AGAAATTAAC	TATGAGATGATGATATTAATGAGAAATCTCAAGATPATGTCCAGAAC	692				
619	CTAATTTCAAC	TAAAGATGATGATATTAACAGAGATTTTCAAGATPATGTCCAGAAC	678				
693	TGTACGAGCTT	CATGAGCTTGTCTGCTGTTTATTCCTCGATGATTACGAGCAATATGACA	752				
679	TGTTCAAGAT	TTCCAAACGCTCTCTCTTTATTCCTGAGATGGTGTGGATATGACCG	738				
753	TCTTCTGATTT	CGAAATGACAGACGCGGCTTTATTTCTACCTTCTCTATAGAC	812				
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813	TTTGGAGACCC	TCAGCTTCCGACACCATCTCTTGGATTACAGCTTACTTCCACAG	872				
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Db 859 TCCTCCTTGATGCTGCTCATCTGTATGTACAGAAGAGCCGAAATCAGCCTAGCAGGC 918
Oy 933 CTGCGAAGCTC 942
Db 919 CCAGCAACAC 928

Search completed: November 5, 2000, 23:47:22
Job time: 32641 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 5, 2000, 16:00:31 ; Search time 54.63 Seconds
(without alignments)
3100.685 Million cell updates/sec

Title: US-09-206-132-1

Perfect score: 1120

Sequence: 1 CACAGGCTGAAGCTTGTCT.....AGAGTAAGCCCAAAAAA 1120

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 262060 seqs, 75620727 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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7: /cgn2_6/ptodata/2/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1120	100.0	1120	4	US-08-101-624-1
3	1120	100.0	1120	5	US-08-479-744A-1
4	1120	100.0	1120	6	PCT-US95-02576-22
5	1014.8	90.6	1161	6	PCT-US95-02576-24
6	995.8	88.9	1428	6	PCT-US94-09642-1
7	407.2	36.4	1151	3	US-08-456-104-3
8	407.2	36.4	1151	6	PCT-US95-02576-20
9	407.2	36.4	1151	6	US-08-479-744A-22
10	394	35.2	1261	6	PCT-US95-02576-12
11	325.2	29.0	330	5	US-08-479-744A-44
12	306	27.3	306	5	US-08-479-744A-46
13	210	18.8	210	6	PCT-US95-02576-31
14	124	11.1	124	6	PCT-US95-02576-39
15	53	4.7	195	6	PCT-US95-02576-41
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18	39.6	3.5	627	1	US-08-449-315-23
19	39.6	3.5	627	1	US-08-449-803-23
20	39.6	3.5	627	1	US-08-449-043-23
21	39.6	3.5	627	2	US-08-456-265A-23
22	39.6	3.5	627	2	US-08-455-416-23
23	39.6	3.5	627	2	US-08-455-244-23
24	39.6	3.5	627	2	US-08-454-876-23
25	39.6	3.5	627	3	US-08-457-364-23
26	39.6	3.5	627	3	US-08-456-262-23

C 27	39.6	3.5	627	3	US-08-456-240-23	Sequence 23, Appl
C 28	39.6	3.5	627	3	US-08-455-736-23	Sequence 23, Appl
C 29	39.6	3.5	627	4	US-08-971-217-23	Sequence 23, Appl
C 30	37.4	3.3	1201	1	US-08-181-271A-26	Sequence 26, Appl
C 31	37.4	3.3	1201	1	US-08-449-315-26	Sequence 26, Appl
C 32	37.4	3.3	1201	1	US-08-444-803-26	Sequence 26, Appl
C 33	37.4	3.3	1201	1	US-08-449-043-26	Sequence 26, Appl
C 34	37.4	3.3	1201	2	US-08-456-265A-26	Sequence 26, Appl
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C 37	37.4	3.3	1201	2	US-08-454-876-26	Sequence 26, Appl
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C 40	37.4	3.3	1201	3	US-08-456-240-26	Sequence 26, Appl
C 41	37.4	3.3	1201	3	US-08-455-736-26	Sequence 26, Appl
C 42	37.4	3.3	1201	4	US-08-971-217-26	Sequence 26, Appl
C 43	36.8	3.3	966	1	US-08-181-271A-24	Sequence 24, Appl
C 44	36.8	3.3	966	1	US-08-449-315-24	Sequence 24, Appl
C 45	36.8	3.3	966	1	US-08-444-803-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-08-456-104-1
Sequence 1, Application US/08456104
Patent No. 5861310

GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.

TITLE OF INVENTION: Tumor Cells Modified to Express B7-2 and B7-3 with Increase

CORRESPONDENCE ADDRESS: 8
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08456, 104
FILING DATE:
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/101, 624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109, 393;
APPLICATION NUMBER: 19-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36, 207
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-456-104-1


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Db 241 TCAAAACCAAGCTGAGTGAAGTATATTTGGCAGGACGAGAAACTTGTCT 300
OY 301 GAATGAGTATATAGGCAAGAAATTTGACAGTGTTCATTTCCAGATATGGCCG 360
Db 301 GAATGAGTATATAGGCAAGAAATTTGACAGTGTTCATTTCCAGATATGGCCG 360
OY 361 CACAAGTTTATTCGACAGTGTGACCTGAGACTTCACATCTTCAGATCAAGACA 420
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Db 421 GGGCTGTATCATATGATCATCCATCAAAAACCCACAGATGATGGCATCCACA 480
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Db 541 TAATATACAGAAATGTGTACATTAATTTGACTGCTCATCTACAGGTTACCCAGA 600
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Db 601 ACCTAAGAGATGAGTGTGCTTGTAGAACCAAGATTCACATTCAGATGATGAT 660
OY 661 TATGAGAAATCTCAAGATATGTACAGAACTGATGAGAGTTCATCAGCTTGTCT 720
Db 661 TATGAGAAATCTCAAGATATGTACAGAACTGATGAGAGTTCATCAGCTTGTCT 720
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Db 721 TTCAATCCCTGATGTACAGCAATATGACATCTCTGATTTCTGGAATCAGACA 780
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RESULT 4
 PCT-US95-02576-22
 Sequence 22, Application PC/TUS9502576
 GENERAL INFORMATION:
 APPLICANT:

TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
 TITLE OF INVENTION: And Uses Therefor
 NUMBER OF SEQUENCES: 65
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA

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ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02576
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120CPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
PCT-US95-02576-22

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Query Match 100.0%; Score 1120; DB 6; Length 1120;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
PCT-US95-02576-24
Sequence 24, Application PC/TUS9502576
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02576
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BMT-1200PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 148..1134
PCT-US95-02576-24

Query Match 90.6%; Score 1014.8; DB 6; Length 1161;
Best Local Similarity 99.8%; Pred. No. 1.8e-287;
Matches 1016; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 204 GCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 263
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Db 384 TTCCAGATATATGGCCGACCAAGTTTGAATGAGAGCTTGAACCTGAGACTTCAAA 443
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Db 444 TCTTGAATCAAGAGCAAGGCTGTATCAATGATATCATCATCAAAAGGCCACAGG 503
Qy 463 AATGATTCGATCCACAGATGATATGATGATGATGATGATGATGATGATGATGATGAT 522
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Qy 523 TGAATATGATCCAAATTTCTAATATTAAGAGAAATGTATCAATTAATTTGACCTGCTATC 582
Db 564 TGAATATGATCCAAATTTCTAATATTAAGAGAAATGTATCAATTAATTTGACCTGCTATC 623
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Db 624 TATPACAGCTTACCCAGAACTTAAGAAATGAGTGTGTTGCTAAGAACCAAGAAATTCAC 683
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Db 864 TCAGCTCCCGCAGACCAATCCTGATGATGATGATGATGATGATGATGATGATGATGAT 923
Qy 883 TGTGATGTTTCTGTCTAATCTATGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 942
Db 924 TGTGATGTTTCTGTCTAATCTATGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 983

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DB 984 TTATAATGTGGAACAACAATGAGAGGAGAGTGAACAGACCAAGAAAAGAGA 1043
OY 1003 AAAAAATCCATATACCTGAAGATCTGATGAAGCCAGCGTGTTTTAAAGTTGGAAGC 1062
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DB 1044 AAAAAATCCATATACCTGAAGATCTGATGAAGCCAGCGTGTTTTAAAGTTGGAAGC 1103
OY 1063 ATCTTCATGCGACAAAGTGTATCATGTCTTTTAAATTAAGATGAAGCCCAAAAAA 1120
|||
DB 1104 ATCTTCATGCGACAAAGTGTATCATGTCTTTTAAATTAAGATGAAGCCCAAAAAA 1161

RESULT 6
PCT-US94-09642-1
Sequence 1, Application PC/TUS9409642
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Purified Mammalian CTLA-4 Binding
TITLE OF INVENTION: Protein and Related Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation, W-3-W
STREET: One Giralda Farms
CITY: Madison
STATE: New Jersey
COUNTRY: USA
ZIP: 07940-1000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh IIfx
OPERATING SYSTEM: System Software 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09642
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/120,606
FILING DATE: 13-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,882
FILING DATE: 03-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Blasdale, John H. C.
REGISTRATION NUMBER: 31,895
REFERENCE/DOCKET NUMBER: DX0390K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-822-7398
TELEFAX: 201-822-7039
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1428 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 152..1123
PCT-US94-09642-1

Query Match... 88.98; Score 995.8; DB 6; Length 1428;
Best Local Similarity 99.88; Pct. No. 7.2e-282;
Matches 997; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 147 GCACATGAGGAGCTGAGTAACATCTCTTTGAGAGGCTTCGCGCTCGTGGTGCATC 206
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OY 180 CTCGAGATTCAGAGCTTATTTCAATGAGAGCTGAGACCTGCATGCCATTTGCAACT 239
|||

DB 207 CTCGAGATTCAGAGCTTATTTCAATGAGAGCTGAGACCTGCATGCCATTTGCAACT 266
OY 240 CTCGAGATTCAGAGCTTATTTCAATGAGAGCTGAGACCTGCATGCCATTTGCAACT 299
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DB 267 CTCGAGATTCAGAGCTTATTTCAATGAGAGCTGAGACCTGCATGCCATTTGCAACT 326
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OY 420 AGGCTGTATCAATGATGATCATCATCAACAAAGCCACAGAAATGATTCGATCCAC 479
|||
DB 447 AGGCTGTATCAATGATGATCATCATCAACAAAGCCACAGAAATGATTCGATCCAC 506
OY 480 AGATGAATTCGAACTGCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 539
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DB 507 AGATGAATTCGAACTGCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 566
OY 540 CTATATATACGAAATGCTGATCAATTAATTTGACCTGCTGCTGCTGCTGCTGCTGCTG 599
|||
DB 567 CTATATATACGAAATGCTGATCAATTAATTTGACCTGCTGCTGCTGCTGCTGCTGCTG 626
OY 600 AACCTAAGAGATGAGTGTCTTCTTAAGAACCAAGAAATTCATCATGATGATGCTA 659
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DB 627 AACCTAAGAGATGAGTGTCTTCTTAAGAACCAAGAAATTCATCATGATGATGCTA 686
OY 660 TTATGCAAGAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 719
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DB 687 TTATGCAAGAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 746
OY 720 TTATGCAAGAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 779
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OY 780 CGGCGCTTTATCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 839
|||
DB 807 CGGCGCTTTATCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 866
OY 840 ACATTCCTTGGATTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 899
|||
DB 867 ACATTCCTTGGATTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 926
OY 900 TAAATCTATGGAATGGAAG 959
|||
DB 927 TAAATCTATGGAATGGAAG 986
OY 960 ACACATGAG 1019
|||
DB 987 ACACATGAG 1046
OY 1020 AAAGATCTGATGAG 1079
|||
DB 1047 AAAGATCTGATGAG 1106
|||
OY 1080 GTGATACATGTTTTTAAATTAAGAGTAAGCCCAAAAAA 1118
|||
DB 1107 GTGATACATGTTTTTAAATTAAGAGTAAGCCCAAAAAA 1145
|||

RESULT 7
US-08-456-104-3
Sequence 3, Application US/08456104
Patent No. 5861310
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nedley, Lee M.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE
NUMBER OF SEQUENCES: 8

D_b 935 TGGAAAGGAGATTACAGCTTCAGTTACTGTGGCCCTCCTCCTTGTGATGCTGCATCATTCATT 994
Q_Y 899 CTAATTCATGGAATGSAAGAAGAGCGGCCCTGCAATC 942
D_b 995 GTATGTCACAGAAAGCCCAATCACGCTTAGCAGAGGCCACAGCAAC 1038

RESULT 11
US-08-479-744A-44
Sequence 44: Application US/08479744A
Patent No. 6084067
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 6084067/1 CTL4/CD28 Ligands and
TITLE OF INVENTION: Uses therefor
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESSES:

Query Match	29.0%	Score 325.2;	DB 5;	Length 330;
Best Local Similarity	99.1%	Pred. No. 4,8e-86;		
Matches 327;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0;

236 AACCTCAAAACCAAGCCGTAGTGAGCTAGTACTATTTTGGCAGGACCAAGAAAACTTG 295

Db	61	AACTCGAAAAACCAAGCGCTAGTGAGCTAGTACTATTTTGGCAGGACCGAAAAACTTG	120
QY	296	GTTCTGATGAGCTATACCTTAAGGCAAAAGAAATTTACAGTGTTCATTCOAAAGTATATG	355
Db	121	GTTCGTGATGAGGATATCTTAAGGCAAAAGAGAAATTTACAGTGTTCATTCOAAAGTATATG	180
QY	356	GGCGCGACAAGTTTGTGATTCGAGTCAGTCAGTGGACCCCTGAGACTTCACAACTTCAGATCAAG	415
Db	181	GGCGCGACAAGTTTGTATTCGAGATGTTGGACCTTGAGACCTTGACAACTTTCAGATCAAG	240
QY	416	GACCAAGGCGTTGTATCAATGATATCATCCATACAAAAAGCCCAAGAGATGATTCGCATC	475
Db	241	GACCAAGGCGTTGTATCAATGATATCATCCACAAAAAGCCCAAGAGATGATTCGCATC	300
QY	476	CACCAATGAAATTCGAACTGCATGCTCT	505
Db	301	CACCAATGAAATTCGAGCTGTACAGTCTCT	330

```

RESULT 12
US-08-479-744A-46
; Sequence 46, Application US/08479744A
; Patent No. 6084067
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: Nos. 6084067e1 CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,744A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/280,757
; FILING DATE: 26-JUL-1994
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 28-AUG-1993
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 306 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..310
;
US-08-479-744A-46

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 5, 2000, 16:26:41 : Search time 79.92 Seconds
(without alignments)
5264.542 Million cell updates/sec

Title: US-09-206-132-1
Sequence: 1 CACAGGCTGAAGCTTTGCT.....AGAGTAAAGCCCAAAAAA 1120

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: N.Geneseq.36.*
2: /SID6/gcgdata/geneseq/geneseqn/NA1980.DAT.*
3: /SID6/gcgdata/geneseq/geneseqn/NA1981.DAT.*
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21: /SID6/gcgdata/geneseq/geneseqn/NA1999.DAT.*
22: /SID6/gcgdata/geneseq/geneseqn/NA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1120	100.0	1120	16	Q81351 Human B lymphocyte
2	1120	100.0	1120	18	T49181 Human B lymphocyte
3	1120	100.0	1120	20	V55784 Human B7-2 antigen
4	995.8	88.9	1424	21	Z29321 Human B7-2 cDNA.
5	995.8	88.9	1428	16	Q85873 B7-2 type B antigen
6	972	86.8	972	20	V83208 B7-2 cDNA. Homo S
7	753.2	67.2	831	19	V03230 DNA encoding CD86
8	723.4	64.6	738	20	V80293 Human B7-2 extrace
9	597	53.3	1897	20	Z27913 Canine B7-2 protel
10	597	53.3	1897	20	Z27914 Canine B7-2 gene c
11	575.2	51.4	987	20	Z27915 Canine B7-2 protel
12	575.2	51.4	987	20	Z27916 Complementary stra

13	566.4	50.6	764	18	T62939
14	558.6	49.9	2830	20	Z27929
15	558.6	49.9	2830	20	Z27930
16	540	48.2	996	20	Z27931
17	540	48.2	996	20	Z27932
18	533.2	47.6	1080	21	Z34838
19	533.2	47.6	1080	21	Z34785
20	468.2	41.8	1795	20	Z27921
21	468.2	41.8	1795	20	Z27922
22	463.8	41.4	840	20	Z27923
23	463.8	41.4	840	20	Z27924
24	407.2	36.4	1151	20	V55785
25	407.2	36.4	1163	18	T49182
26	405.6	36.2	1163	16	Q81366
27	397	35.4	403	20	V89569
28	394	35.2	1261	16	T01046
29	369.2	33.0	942	19	T99926
30	325.2	29.0	330	18	T49197
31	306	27.3	306	18	T49198
32	212.6	19.0	509	20	Z27933
33	212.6	19.0	509	20	Z27934
34	210	18.8	210	16	T01038
35	124	11.1	124	16	T01045
36	110	9.8	359	20	Z27935
37	110	9.8	359	20	Z27936
38	53	4.7	195	16	T01072
39	39.6	3.5	627	20	V62819
40	39.6	3.5	627	20	V81612
41	37.4	3.3	1201	20	V62822
42	37.4	3.3	1201	20	V81615
43	36.8	3.3	966	20	V62820
44	36.8	3.3	966	20	V81613
45	36.8	3.3	1204	11	Q06200

ALIGNMENTS

Chimeric human/por
Feline B7-2 protel
Feline B7-2 gene c
Feline B7-2 protel
Complementary stra
Feline CD86 (B7-2)
Cat CD86 (B7-2) CD
Canine B7-25 prote
Canine B7-25 gene
Canine B7-25 prote
Complementary stra
Mouse B7-2 antigen
Mouse B lymphocyte
Murine B lymphocyt
EST clone CR506.
Mouse B7-2 exons m
Rat CD86 coding se
Human B lymphocyte
Human B lymphocyte
Feline B7-2 protel
Feline B7-2 gene (h
Human B7-2 exon 5.
Human B7-2 exon h1
Feline B7-2 protel
Feline B7-2 gene (h
Human B7-2 exon h1
Tobacco PR-2 gene
PR-O protein encod
Tobacco PR-2 gene
PR-2' protein enc
Tobacco PR-2 gene
PR-N protein encod
PR-2 cDNA cloned 1

RESULT 1	Q81351	standard; cDNA: 1120 BP.
ID	Q81351	
AC	Q81351	
DT	20-AUG-1995	(first entry)
DE	Human B lymphocyte antigen B7-2 (hB7-2-clone 29).	
XX		
KW	CTLA4/CD28; counter receptor; B lymphocyte antigen; B7-2; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	107..1093
FT		/*tag= a
XX		
PN	W09503408-A.	
XX		
PD	02-FEB-1995.	
XX		
PF	26-JUL-1994.	94WO-US08423.
XX		
PR	26-JUL-1993.	93US-0101624.
PR	19-AUG-1993.	93US-0109393.
PR	03-NOV-1993.	93US-0147773.
XX		
PA	(DAND) DANA FARBER CANCER INST INC.	
PA	(REPK) REPLIGEN CORP.	
XX		
PI	Freeman GJ, Gray GS, Greenfield E, Nadler LM;	
XX	WPI: 1995-075236/10.	
DR	P-PsDB; R67984.	

Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful for enhancing or suppressing T-cell mediated Immune responses

Claim 4; Fig 8; 175pp; English.

Claim 4; Fig 8; 175pp; English.

CC A cDNA library was constructed in the pCDM8 vector using poly A⁺ RNA
CC from the human anti-IGM activated B cells. Four clones were strongly
CC positive for B7-2 expression by indirect immunofluorescence using
CC Cyt4A4 and flow cytometric analysis. The B7-2 cDNA insert in clone
CC 29 was sequenced in the pCDM8 expression vector employing the
CC following strategy. Initial sequencing was performed using
CC sequencing primers T7 (081352), CDM8R (081353) (Invitrogen) homologous
CC to pCDM8 vector sequences adjacent to the clone B7-2 cDNA. Sequencing
CC was performed using dye terminator chemistry and an ABI automated DNA
CC sequencer. DNA sequence obt. using these primers was used to design
CC additional sequencing primers (see 081354-081353). This cycle of
CC sequencing and selection of additional primers was continued until
CC the B7-2 cDNA was completely sequenced on both strands. The human
CC B7-2 clone 29 cDNA sequence is given in 081351. The predicted
CC protein sequence (R67984) exhibits many features common to other
CC type 1 Ig superfamily membrane proteins. Following cleavage of the
CC signal peptide the resulting membrane-bound protein would have an
CC unmodified mol. wt. of approx. 34 kDa. The extracellular domain
CC contains eight potential N-linked glycosylation sites. E. coli
CC transfected with a vector contg. the cDNA insert of clone 29 was
CC deposited under ATCC 69357 on July 26 1993.

Sequence 1120 BP; 354 A; 237 C; 230 G; 299 T; 0 other;

Query Match	100.0%;	Score 1120;	DB 16;	Length 1120;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1120; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY	1	CACAGGGGTGAACCTTTGGCTTCCTCCCTCTTAACAGAGACTTGACACAGCAACAGAT	60
Db	1	cacaggggtgaacgctttgcttctcctccttgaacagagacttgacacagacacagat	60
OY	61	GAGTGGGGTCATTTCACGATATTAGGTCACACAGAGACGCCAAATAATGATCCCGCATG	120
Db	61	gagtgggggtcatttccacgattattaggtccacagcagaagcagccaatatgattccccagtg	120
OY	121	CACATGGGAGCTCAGTAAACATTCCTCTTGGATGGGCTTCCTGCMCTGGTGGTGGTCC	180
Db	121	caecatgggagctcagtaaacattctctcttggatgggcttccctgcctctccctggtgctgc	180
OY	181	TCTGAAGATTCAAGCTTTATTTTCATGAGACTGCACACCTGGCATGCCAATTTGGAACTC	240
Db	181	tcctgaagattccaagcttattccaatgagagctgcgacactgcctgcatgcacatgttgaaactc	240
OY	241	TCAAAACCAAAAGCCTGAGTGAGCTAGTACTGATATTTTGGCAGACACAGGAAAATTGGTTCT	300
Db	241	tcaaaaccaaagcctgagtgagctagtagtatttttggcagacacaggaanaaactggttct	300
OY	301	GAATGAGGATCTACTCTTGGCGAAAGAGAAATTTACAGCTTTGATTTCCAGATATAGGGCCG	360
Db	301	gaatgaggtactactcttgccaagagaataattgacagtggttcaatcccaagtatatggccg	360
OY	361	CACAAGTTTTGATTGSGAGATTGGACCCCTGAGACTTCACAACTTCAGATTCAGATCAAGGACAA	420
Db	361	cacaagtttggatttgsgagattggacccctgagacttcacaacttcagatcaagagcaa	420
OY	421	GGGCTTGTATCATATGATTCATCCATCACAAAAGCCCAAGAGATGATGGATCCACCA	480
Db	421	gggcttgtatcatatgattcatccatcacaaaagcccaagaaatgattgcacaccaca	480
OY	481	GATGAATTCTGAACCTCTCAGTGGCTGGCTCAACTTCAGTCAACCTTAATAATAGACCAATTTC	540
Db	481	gatgaattctgaacctctcagtggtcgtgctaactcagtcgaacctgaaataglaccaatttc	540
OY	541	TAAATATACGAAAATGTGTACATAAATTTGACCTGCTCATCTATPACAGGTTACCCGA	600
Db	541	taaatatacgaaaaatgtgtacataaattttgacctgctcatctatpacaggttacccca	600

[illegible]

CC of MHC class II and co-stimulatory molecule B7 can be manipulated by
 CC regulating the intracellular dissipation of proton motor force which can
 CC be assessed in terms of mitochondrial membrane potential. These methods
 CC can be used for regulating cell growth and division to control disease
 CC processes by manipulating mitochondrial metabolism and the expression of
 CC cell surface immune proteins. They can be used for treating diseases
 CC associated with excessive cellular division, aberrant differentiation,
 CC and premature cellular death, e.g. cancers, autoimmune diseases,
 CC neurodegenerative disorders etc.

XX Sequence 1424 BP; 429 A; 306 C; 284 G; 405 T; 0 other;

Query Match 88.9%; Score 995.8; DB 21; Length 1424;

Best Local Similarity 99.8%; Pred. No. 1,7e-288;

Matches 997; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 120 GCACATGAGGAGTGAACATCTCTTGTGATGGCTTCTGCTGCTGCTGCTGCTC 179
 |||||||
 DB 143 gcaatgagtgactgagtaacatctcttcttgatggcctctctctctgctgctgctc 202
 OY 180 CTCTGAGAGTTCAGAGCTTATTTCAATGAGACTGACAGCTGCAATGGCAATTTGCAAACT 239
 |||||||
 DB 203 ctctgaagatccaagcttattctcaatgagactgagactgagactgagactgagactgagact 262
 OY 240 CTCAAAACCAAGCCTGAGCTAGTACTAGTATTTGGCAGACGACGACGACGACGACGACGACGAC 299
 |||||||
 DB 263 ctcaaaaccaaagcctgagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 322
 OY 300 TGAATGAGGTACTTGAAGCAAGAAATTTGACAGCTTCAATTCACATATATATGAGGCTC 359
 |||||||
 DB 323 tgaatgaggtacttacttaggcaagaagaattgacagtgctcatctccaaagtatagtagtagtagtag 382
 OY 360 GCACAAATTTGATTTGAGACAGTTGACCTGAGACTTCAATCTTCAATCTTCAATCTTCAATCTTCA 419
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 DB 383 gcaacaatttgatctgagacagctgagacccgagacccgagacccgagacccgagacccgagacccgag 442
 OY 420 AGGCTTGTATCATGTATCATCATCATCAAAAGCCACAGAGATGATGATGATGATGATGATGATGATG 479
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 DB 443 agggcttgatcat 502
 OY 480 AGATGAATTTGAGACTGAGCTGCTTGTAACTTCACTCAACCTGAAATTAATTAATTAATTAATTAAT 539
 |||||||
 DB 503 agatgaatttcgaactgacgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 562
 OY 540 CTAAATATACGAAATATGATATTAATTTGACCTGCTCATATATATATATATATATATATATATATAT 599
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 DB 563 ctaataacagaagaattgtacataaatttgacctgctcatcatcatcatcatcatcatcatcatcatcat 622
 OY 600 AACCTAAGAGTGAAGTGTGTTTGTGAAGACCAAGAAATTAATTAATTAATTAATTAATTAATTAATTA 659
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 DB 623 aacctaaagaagaatgagtgcttctgctcaaaacaaacaaacaaacaaacaaacaaacaaacaaacaaac 682
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 DB 683 ttaigcagaatctcaagataatgtcacagactgtacagactgtacagactgtacagactgtacagactgt 742
 OY 720 TTTTCATTTCCCGATTTACGAGCAATATGACCATTTTGTATTTGCAAACTGACAGCA 779
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 DB 743 ttctcatccctgagtgctgagcaataatgacacatctctgattcttctgaaactgacagaga 802
 OY 780 CGCGGCTTTTCTTCACCTTCTCTATAGAGCTTGAAGACCTGACCTGACCTGACCTGACCTGACCTGAC 839
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 DB 803 cggcgcttctacatctcctctctcatagagcttgaagacccctcagccctcccccagacc 862
 OY 840 ACATTCCTTGGATTAACAGCTGACTTCCACAGATTAATATATATATATATATATATATATATATATATAT 899
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 DB 863 aatttccttggttacagctgacttccacagatattatattggtggtggtggtggtggtggtggtggtggtg 922
 OY 900 TAAATCTATGGAATGGAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 959
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 DB 923 taattctatgaaatcgaagaagaagaagcggcctcgaacatctatataatggtgaaacca 982

OY 960 ACACATGAG 1019
 |||||||
 DB 983 acccaag 1042
 OY 1020 AAAGATCTGATGAAGCCACGCTGTTTAAAAGTTGCAAGACATCTTATGCGACAAA 1079
 |||||||
 DB 1043 aaagatctgtagagccagcagctgtttttaaagttcgaagacatcttcatcgcagcaaaa 1102
 OY 1080 GTGATCATGTTTATTAATTAAGAGTAAAGCCCAAAAA 1118
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 DB 1103 gtagacatgltttaaattaaagagaaagccataca 1141

RESULT 5

085873

ID 085873 standard; cDNA: 1428 BP.

XX 085873;

XX 09-OCT-1995 (first entry)

DE B70 type B antigen which binds CTLA-4 and CD28.

KW B70 antigen; CTLA-4; CD28; T cell response; ss.

XX Homo sapiens.

OS Homo sapiens.

FT CDS

FT 152..1123

PN MO9506738-A.

XX 09-MAR-1995.

XX 02-SEP-1994; 94MO-US09642.

XX 03-SEP-1993; 93US-0116882.

XX 13-SEP-1993; 93US-0120606.

PA (AZUM/) AZUMA M.

PA (OKUM/) OKUMURA K.

XX (SCHE) SCHERING CORP.

PI Azuma M, Lanier LL, Okumura K, Phillips JH;

PI Somoza Diaz-Sarmiento M;

DR P-PSDB; R71478.

XX WPI; 1995-115453/15.

XX New CTLA-4/CD28 binding protein, B70 - used to develop prods for

PT modulating the physiology, growth or development of cells.

XX Claim 12; Page 42-44; 55pp; English.

XX B70 is a natural proteinaceous binding partner for CTLA-4 and CD28

XX markers/antigens. It is distinct from the known B7/BH1 marker. It is

XX representative of 'type B' markers/antigens/binding partners. The

XX type A markers/binding partners include both CTLA-4 and CD28 and

XX antibodies specific for B70, and are characterised, in part, by the

XX property of serving as a binding partner for B70. A cDNA encoding a

XX B70 antigen was cloned by expression cloning using mAb 172.236 to

XX select COS7 cells transfected with a cDNA library cloned into the

XX pURE4 vector. The library was made from RNA isolated from a human

XX EBV-transformed B-lymphoblastoid cell line JY.

XX Sequence 1428 BP; 432 A; 306 C; 285 G; 405 T; 0 other;

Query Match 88.9%; Score 995.8; DB 16; Length 1428;

Best Local Similarity 99.8%; Pred. No. 1,7e-288;

Matches 997; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

1
QY 120 GCATATGAGCATGATACATTCCTTTGATGAGCCTTCCTGCTCTCTGCTGCTC 179
DB 147 gcatataggagctgagtaaacctctcttgtagggccttcctcctcgtgctgc 206
QY 180 CTCTGAAGATCAAGCTTATTTCATGAGACTGCAGACCTGCCATTTGGCAACT 239
DB 207 ctctgaagatcaagcttatttcaatgagactgcagactgcagatgccaatltgnaact 266
QY 240 CTCAAAACCAAGCTGAGTACAGTACTAGTATTTGGCAGAGCAGCAAACTTGCTC 299
DB 267 ctcaaaccaagcctcgtgagctagtagtatttggcagagcacaagaaacttgctc 326
QY 300 TGAATGAGTACTTGGCAAGCAAAATTTGACAGTGTTCATCTCCAACTATATGGCC 359
DB 327 tgaatgagtactacttggcacaagaatttgacagtggttcatctccagatattggcc 386
QY 360 GCACAAGTTTGAATCGACAGTTGACCTGAGACCTTACAAATCTTCAGATCAAGACA 419
DB 387 gcacaagtttgatcgtgacagctggaccctgagactcacatctcagatcaagaca 446
QY 420 AGGCTGTATCATGATATCATCATCAAAAAGCCACAGCAATGATTTGGCATCCACC 479
DB 447 aggctgtatcaatgatacatccacaagaagccacaggaatgattcgcacacc 506
QY 480 AGATGAATTCGAACCTGCTGCTGCTTAATTCAGTCAACCTGAATAGTACCAATTT 539
DB 507 agatgaattctgaaactcgaatgctgtctgaacttcagtcacacccgaaatgatacaatt 566
QY 540 CTATATTAACAGAAATGTGTACTAAATTTGACCTGCTCATTAACACGGTTACCCAG 599
DB 567 ctataataacagaaatggtacataaattgacactgcacatcacaagcttaccag 626
QY 600 AACCTAAGAAGATGATGTTTGGTAAAGAACCAAGATTCACATGAGAGATATGTTA 659
DB 627 aacctaagaagatgagtggttggtaagaagaattcacaatcagatcagatgagta 686
QY 660 TTAATGCAAAATCTCAAGATTAATGTACAGAACTGTACAGAGTTTCATCAGCTTGTCTG 719
DB 687 ttatgcagaatctcaagaataatgtcacagactgtacgagcttcatcagcttgctg 746
QY 720 TTTTCATCCCTGATGTTACAGAGCAATATGACATCTTCTGATTTCTGGAACCTACAAAGA 779
DB 747 ttctatccctgagtgtaacgagaataatgacatctctgtattcttgaaactgacaga 806
QY 780 CGCGGCTTTATCTTACCTTCTCTATAGAGCTTGAAGACCTCAGCCTCCCCAGACC 839
DB 807 cggcgctttatcttccacttctctatagagcttgagaccctcagcctcccccagacc 866
QY 840 ACATTCCTTGATTAACAGCTGTACTCCAAAGTTATATATGTGATGGTTTCTGTC 899
DB 867 acattccttgatatacagctgtacttccacaagttatataatgtagtatttctgctc 926
QY 900 TAAATTCATGGAATGGAAGAAGAAAGGGCTCCCAACTCTTATTAATGTGGAACCA 959
DB 927 taattctatggaatggaagaagaagaagcgctcgaactcttataaaltgtagaacca 986
QY 960 ACACAATGAGAGGAGAGAGAGTGAACAGACCAAGAAAGAAAGAAATCCATTTACCTG 1029
DB 987 acacaatgagagaggaagagagtgtaacagaccaaagaagaagaaatccatataccctg 1046
QY 1020 AAAGATCTGATGAAGCCACGCTGTTTAAAGTTGGAAGACATCTTCGCACAAAA 1079
DB 1047 aaagatctgtagaagccacgctggtttttaaagttcgaagacatcttcatgcaaaaa 1106
QY 1080 GTGATACATGTTTAAATTAAGAGTTAAGCCCAAAAA 1118
DB 1107 gtgatacatggtttttaaataaagataaagccatacaa 1145

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RESULT 6
 ID V83208
 V83208 standard: cDNA: 972 BP.
 XX

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AC V83208:
XX 02-MAR-1999 (first entry)
DT B7-2 cDNA.
XX
DE
XX
KW Mouse; immunodeficient; pathogen; tumour; lymphocyte; antigen;
KW immunomodulator; vector; vaccine; cancer; HIV; leishmania;
KW Mycobacterium; listeria; plasmidium; retrovirus; evaluation;
KW human immunodeficiency virus; ds.
XX
OS Homo sapiens.
XX
PN M09844788-A2.
XX
PD 15-OCT-1998.
XX
PF 09-APR-1998; 98WO-US06944.
XX
PR 09-DEC-1997; 97US-0069163.
PR 09-APR-1997; 97US-0838702.
PR 01-MAY-1997; 97US-0848760.
XX
PA (CHAN/) CHANG L.
XX
PI Chang L.
XX
DR WPI: 1999-024005/02.
XX
PT Use of immunodeficient mice comprising human cells - particularly
PT SCID/Beige mice comprising human immune cells for evaluating
PT vaccines against cancers or human pathogens, e.g. HIV
XX
PS Example 1b: Page 104-105; 154pp; English.
XX
CC Immunodeficient mice comprising human cells can be used for
CC exposure to human pathogens and/or their components or human
CC tumour cells and human peripheral blood lymphocytes. Also claimed
CC is a vaccine comprising a cell modified to express an antigen and
CC an immune-modulating protein, this is preferably an expression
CC vector comprising a polynucleotide sequence that encodes the
CC antigen and immune-modulating protein. Such vectors can be used
CC to treat a subject having a tumour by transferring the expression
CC vector into the tumour so that the antigen and the immune-modulator
CC are expressed by at least the tumour. The methods can be used for
CC producing and evaluating vaccines including cancer vaccines and
CC vaccines directed against human pathogens, e.g. HIV, leishmania,
CC Mycobacterium, listeria or plasmidium. This sequence is an
CC intermediate retroviral vector derived from pLNL6, a vector approved
CC for clinical use in the United States. pLNL6 is essentially pLNL6
CC digested with ClaI and BclI to remove cloning sites and the pLNL6
CC internal Sneo gene. These were replaced with a polylinker. A neo
CC gene was then inserted under the transcriptional control of the SV40
CC enhancer/promoter to create the vector pLSN. Two primers (V83187,
CC V83188) were used to amplify the B7-2 cDNA (a ligand for
CC CD28/CTLA-4 proteins, co-stimulators for interleukin-2 driven
CC proliferation of T-cells) for its insertion into pLSN.
XX
XX
SQ Sequence 972 BP; 304 A; 204 C; 194 G; 270 T; 0 other;

```

Query Match 86.8%; Score 972; DB 20; Length 972;
 Best Local Similarity 100.0%; Pred. No. 1.9e-281;
 Matches 972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 125 ATGGAGCTGAGTAACATTCCTTGTGATGAGCCTTCCTGCTCTGCTGCTCTCTG 184
DB 1 atggagctgagtaaacattctcttgtagtgagccttccctcgtctgctcctcctg 60
QY 185 AAGATTCAACCTTATTTCATGAGACTGCAGACCTGCCATGCCAATTTGCAAACTCTCA 244
DB 61 aagattcaagcttatttcaatgagactgcagacctgcacatgccaatttgcaactctcaa 120

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QY 245 AACCAAGCCTGAGTACAGTACTAGTATTTTGGCAGACACAGAAAAGCTGGTTCGAAT 304
    |||||||
Db 121 aaccaaagcctgaagtgaagctagtagtatttggcagagcaccagaaacttgcttgat 180
QY 305 GAGGTATCTTATGCGAAGAAAGAAATTTGACAGTGTTCATTCGAATATATGGCCGAC 364
    |||||||
Db 181 gaggtatctttagcgaagaagaatttgcagtgcttccaaagtataatggccgcaca 240
QY 365 AGTTTTGATTTGGACAGTGTGACCCCTGAGACTTCACAAATCTTCAGATCAAGACAGG 424
    |||||||
Db 241 agtttgcatttcggaacagctggaccttgagatcctcacaatcctcagaagcaagg 300
QY 425 TTGTATCAATGTATCATTCATCACAAGAACCCACAGAGATGATTCGATCCACAGATG 484
    |||||||
Db 301 ttgtatcaatgtatcatcctacataaaagccacagagatgatcgcacacagatg 360
QY 485 AATTCTGAACCTGTCAGTGTCTGCTCAACTTCAGTCMAACCTGAATGTACCAATTTCTAT 544
    |||||||
Db 361 aattctgaactgtcagtgcttgcctaaactcagtcgaatgaatgacaaatcttcaat 420
QY 545 ATACAGAAAATGTGTACATTAATTTGACCTGCTCATCTATACAGGTTTACCAGAACCT 604
    |||||||
Db 421 atacagaaaatgtgtacataaaattgacctgtcatctacatacaggttacccagaa 480
QY 605 AAGAGATGAGTGTGTTTGTAGAACCAAGAAATTAAGTATGATGATGATGATGATG 664
    |||||||
Db 481 aagaagatgagtgcttctgtaagaacaaagaaatcgaatcagatgagtatgataatg 540
QY 665 CAGAAATCTCAATATATGTCACAGAACTGTACGAGTTTCCATGAGCTTGTTGTTTCA 724
    |||||||
Db 541 cagaatactcaagaataatgtcacagaactgtacagactccacagcttgcttgcttca 600
QY 725 TTCCCTGATGTGTACGACATATATGACCATCTCTGTATTTCTGGAACCTGACAGCG 784
    |||||||
Db 601 ttccctgatgttacgagcaatagacacatctctgtatcttgcgaactgcaagacg 660
QY 785 CTTTATCTTCACCTTTCTCTATAGAGCTTGAGAGACCCCTAGCCTCCCGACACCAAT 844
    |||||||
Db 661 ctltatcttcacacttctctatagagcttgagagacccctcagcctccccaagaca 720
QY 845 CCTGGATTTACAGCTGACTTCCAAAGTATATATATGATGATGATGATGATGATGAT 904
    |||||||
Db 721 ccttgatctcagctgacttccaaacgtatataatgtagtggttctctgctcaat 780
QY 905 CTATGAATGGAAGAAAGAAAGCGGCTGCGCAACTCTTATTAATGTGGAACCAACACA 964
    |||||||
Db 781 ctatgaaatggaagaagaagaagcgctcgcacactctataaatgttggaaccaacaca 840
QY 965 ATGGAAGGGAAGAGAGTGAACAGACCAAGAAAAGAAAATTCATATACCGGAAGA 1024
    |||||||
Db 841 atggaaggggaagagatgacagacaaagaagaagaataacccatatacctggaaga 900
QY 1025 TCTGATGAAGCCGAGCTGTTTAAAAAGTTCGAAAGACATCTTCATCGACGAAAAGTAT 1084
    |||||||
Db 901 tctgatgaagcccgagctggtttttaaagaagtcgaagaacatctcatgctgcaaaag 960
QY 1085 ACATGTTTTTAA 1096
    |||||||
Db 961 acatgtttttaa 972

```

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KW human; ds.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH sig_peptide 52..126
FT /*tag= a
FT mat_peptide 127..831
FT /*tag= b
XX
XX WC9747732-A2.
XX
XX 18-DEC-1997.
XX
XX 13-JUN-1997; 97WO-0512599.
XX
XX 21-FEB-1997; 97US-0038915.
XX 14-JUN-1996; 96US-0019934.
XX 19-FEB-1997; 97US-0043948.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Chaikin MA, Lyn SDP, Sweet RW, Truneh A;
XX
XX WPI: 1998-052299/05.
XX P-PSDB; W32339.
XX
XX Hexameric fusion protein containing Iga antibody fragment - used for
XX stimulating CD28 positive cells, or suppressing CTLA-4 positive
XX cells
XX
XX Example 1; Fig 5A-B; 105pp; English.
XX
XX This DNA sequence comprises a portion of plasmid CD86calphatplink
XX that codes for the signal region and extracellular domain (see
XX W42339) of human CD86 extracellular domain. The plasmid encodes a
XX fusion protein comprising the CD86 signal peptide and extracellular
XX domain grafted to a human IgG1 heavy chain Fc region and the
XX tailpiece region (alpha-tp) (see W42344) of human Iga heavy chain.
XX The processed fusion protein has been expressed as a hexamer in COS
XX cells. The invention relates to novel hexameric fusion proteins
XX comprising a dimeric binding protein such as CD86 provided at its
XX C-terminus with a tailpiece that has the activity of alpha-tp. The
XX tailpiece provides the fusion protein with the ability to alpha-tp
XX stable hexamers. Also claimed are polynucleotides encoding the
XX hexameric fusion proteins, vectors, recombinant host cells and a
XX method for producing the hexamers. The fusion protein is useful in
XX therapeutics and vaccines, and is particularly well suited for
XX applications for which the binding protein from which it is derived
XX is unsatisfactory because of low binding affinity or for
XX applications where multivalency is desired. Applications include
XX diagnostics, binding assays and screening assays. CD86-Ig-alpha-tp
XX fusion protein is used in claimed methods for stimulating CD28
XX positive cells or suppressing CTLA-4 positive cells.
XX
XX Sequence 831 BP; 247 A; 201 C; 162 G; 221 T; 0 other;

```

Query Match 67 2%; Score 753.2; DB 19; Length 831;

Best Local Similarity 99.0%; Pred. No. 6; 5e-216; Mismatches 8; Indels 0; Gaps 0;

```

QY 81 ATTAGTCACAGCAGAGCAGCAAGCAATGAGTCCCAAGTGCATATGAGTACGATGAC 140
    ||| ||| |||||||
Db 26 attcggtaccagcagaagaagcgaataatgatacccgagtcactatgagactgaataa 85
QY 141 TTCTCTTTGATGAGCCTTCTGCTCTGTGCTGCTCTCTGATGAGATTCGAAGCTTAT 200
    |||||||
Db 86 ttctcttggatgagccttcctcctctctctctctctctctctctctctctctctctct 145
QY 201 TCAATGAGAGTGCAGACCTGCGCATGCCAATTTGCAAACTCTCAAAACCAAGCGTGA 260
    |||||
Db 146 tcaagagacgcagacccctgcacatgccaatttgcgaactctcaaaacaaagcctgag 205

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OY 261 AGCTAGTATATTTGGGAGCAGCAGGAAAATTGTTCTGAATGAGCTATACCTAGGCA 320
DB 206 agctagatgatattttggagagcagagaaaactggtcttgatgagttactatgagca 265
OY 321 AAGGAAATTTGACAGTGTTCATTCAGATATATGAGCCGACAGCAATTTGATTGGACA 380
DB 266 aagagaatttgcagagtggttcaatcagatataagggcgacagagtttgatcgagca 325
OY 381 GTTGGACCTGAGACTTCACATCTTCAGATCAAGAGCAAGGGCTTATCAATGATCA 440
DB 326 gttgagacctgagacttcaacatctcagatcaagagcagggttgatcattgataca 385
OY 441 TCCATCAGAAAAGCCACAGCAATGATTCGATCACCAGATCAATTCGAACTGTACG 500
DB 386 tccatcacaaaagccacaggaatgattcgatccacacagatgaattcgaactgacag 445
OY 501 TGCTTGCTAAGCTGAGTCAACCTGAATAGTACCAATTTCTAATATATACGAAATGTGT 560
DB 446 tgccttgcaacttccagttcaactgaaatagttaccatcttcaatatacagaaaatggt 505
OY 561 ACATTAATTTGACCTGCTCATCTATPACAGGTTACCCAGAACTAGACAGATGAGTGT 620
DB 506 atataaattgacctgcctcactatacaggttaccagagacctaagaatgagtggtt 565
OY 621 TGCTTAAGAACCAAGATTCACATCTGAGTATGATGATGATGATGATGATGATGATG 680
DB 566 tgcataagacaagaatcactatcagatcagatgagttatcagcaaaatccaaagata 625
OY 681 ATGTACAGAACTGTACAGCTTTCATCAGCTTGTCTGTTTATTCCTGATGTTACGA 740
DB 626 atgtcacagaaactgtacgagctgtccatcagctgtctgtctcctgactgactaaga 685
OY 741 GCAATATGACCATCTCTGATTCGTGAAACTGACAGAGCGGCTTTATCTTCACCTT 800
DB 686 gcaataatgacatctctgattctcgtgaaactgacaagacgagctcttcatcttcaact 745
OY 801 TCTCTATAGAGCTTGAGAGACCCCTCAGCCCTCCGACAGACCAATTC 846
DB 746 tctctatagagcttgagagacccctcagccctcccccagacagagcc 791

```

RESULT 8

V80293 standard; cDNA; 738 BP.

V80293;

15-MAR-1999 (first entry)

Human B7-2 extracellular domain and linker DNA.

Tumour interacting protein; cancer; gene therapy; vector;

57A antigen; monoclonal antibody; single chain antibody;

mouse; human; B7-2; co-stimulatory molecule; ss.

Chimeric - Homo sapiens.

Chimeric - synthetic.

W09855607-A2.

10-DEC-1998.

04-JUN-1998; 98WO-GB01627.

04-JUL-1997; 97GB-0014230.

04-JUN-1997; 97GB-0011579.

20-JUN-1997; 97GB-0013150.

(OXFO-) OXFORD BIOMEDICA UK LTD.

Bebington CR, Carroll MW, Ellard FM, Kingsman SM;

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XX MPI: 1999-059910/05.
DR P-PSDB: W86005.
PT New vector encoding a tumour interacting protein for treating cancer
PT - contains a desired nucleotide sequence and/or protein which
PT recognises tumours, and is used as a gene delivery system to treat
PT cancer
XX
PS Example 5; Fig 4; 82pp; English.
XX
CC This DNA sequence encodes a polypeptide (see W86005) comprising
CC the extracellular domain (amino acids 1-215) of human co-stimulatory
CC molecule B7-2 joined to a C-terminal flexible peptide linker. This
CC is part of the coding sequence of B7-2.574.1 co-stimulatory domain,
CC a DNA sequence encoding a fusion protein comprising the B7-2
CC extracellular domain joined via the linker to an scFv (see W86002)
CC derived from murine 574 monoclonal antibody. The cDNA can be
CC inserted into vector pCI to allow expression of the fusion protein
CC in mammalian cells. The trophoblast cell surface antigen defined
CC by 574 is expressed at high levels on the cells of a wide variety
CC of human tumours. The invention relates to a vector comprising a
CC nucleotide sequence coding for a tumour interacting protein (TIP)
CC and optionally a nucleotide sequence of interest (NOI) which
CC encodes a protein of interest (POI), the vector being capable of
CC delivering the NOI and/or POI to the tumour recognised by the TIP.
CC Delivery can be in vivo or ex vivo. The vector is used to treat
CC cancer, and may also be used as a gene delivery system for
CC introducing at least 1 gene encoding a TIP (preferably a tumour
CC binding protein) into a haematopoietic cell lineage. B7-2 is
CC expected to bind specifically to CD28 and CTLA-4 present on human
CC T-cells.
XX
SQ Sequence 738 BP: 215 A; 168 C; 148 G; 207 T; 0 other;

```

Query Match 64.6%; Score 723.4; DB 20; Length 738;
 Best Local Similarity 99.9%; Pred. No. 5.2e-207;
 Matches 724; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 125 ATGGAGCTGAGTAACTCTCTTGTGATGAGCGCTGCTGCTGCTGCTGCTGCTGCTG 184
DB 1 atggagctgagtaactctcttgtgagtgagcgctgctgctgctgctgctgctgctg 60
OY 185 AAGATTCAAGCTTATTTCAATGAGACTGACAGCTGACATGCCAATTTGCAAACTCTCA 244
DB 61 aagattcaagcttattttcaatgagactgacagctgacatgccaatTTGCAAACTCTCA 120
OY 245 AACCAAGCCGAGTGAGTGTAGTATTTTGGCAGGACGAGGAAAAGTGGTCTGAT 304
DB 121 aaccAAGCCGAGTGAGTGTAGTATTTTGGCAGGACGAGGAAAAGTGGTCTGAT 180
OY 305 GAGTATTAAGCTTATTTCAATGAGACTGACAGCTGACATGCCAATTTGCAAACTCTCA 364
DB 181 gagtattAAGCTTATTTCAATGAGACTGACAGCTGACATGCCAATTTGCAAACTCTCA 240
OY 365 AGTTTGATTCGAGCTGAGTGTAGTATTTTGGCAGGACGAGGAAAAGTGGTCTGAT 424
DB 241 agtttgatTCGAGCTGAGTGTAGTATTTTGGCAGGACGAGGAAAAGTGGTCTGAT 300
OY 425 TTGATCAATGATTCATTCATCAAAAAGCCGACAGGAATGATTGCATCCACGAGATG 484
DB 301 ttgatcaatgattcatTCATTCATCAAAAAGCCGACAGGAATGATTGCATCCACGAGATG 360
OY 485 AATTCGAACTGAGTGTAGTATTTTGGCAGGACGAGGAAAAGTGGTCTGAT 544
DB 361 aatTCGAACTGAGTGTAGTATTTTGGCAGGACGAGGAAAAGTGGTCTGAT 420
OY 545 ATAACAGAAATGTGTACATTAATTTGACCTGCTCATATACAGCGTTACCCAGAACT 604
DB 421 ataacagaaatgtgtacatTAATTTGACCTGCTCATATACAGCGTTACCCAGAACT 480
OY 605 AAGAAGATGAGTGTGTTTGTCTAGAACCAAGAAATTCATTCGAGTATGATGATTATG 664

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Query Match	53.3%	Score 597	DB 20	Length 1897
Best Local Similarity	78.2%	Pred. No. 6.4e-169		
Matches 798	Conservative 0	Mismatches 205	Indels 18	Gaps 6

QY	102	CCAAATATGATCCCACTGCTACTGATGGACAGTATACATTTCTTTGTATGGCTTCC	161
Db	1	ccaagatgctatccagatgactgactatggaacttgaataacatctcttctgtatgacccctc	60
QY	162	TGCTCTCTGGTGGTGGCCGCTGGAAGATTCAAGCTTATTATTCATGAGACATGCGACCTGC	221
Db	61	tgcctatggtgcgtcgtctccaatgaagatcaagcatatttcaacaagatccgggaactcgc	120
QY	222	CATGCCAATTTGGCAAACTCTCAAAACCAAAAGCTGATGGTACCTAGTATTTTGGCAGG	281
Db	121	catgcatctttacaattcccaattccaacaataagcctgtgatgtatgttctgttgcgag	180
QY	282	ACCAAGAAACTTGTTCTGTAATGAGCTATTACTTGCGCAAGACAAATTTGACAGTTC	341
Db	181	accagatlaagcttgcgtctgtatgagctatcacagagaaagaaagaaacccctcaaaigtcc	240
QY	342	ATTCAGATATATGAGCGCGACAAAGTTTGTATTCGGACAGTGTGACCTGAGACTTCACA	401
Db	241	atcgcaagtataagggcgccgaacaagctttgtacaagaacaatttggacccttgactccata	300
QY	402	ATCTTCAGATCAAGACAGAGGCTTTGATTCAAATGTAATCATCATCACAAAAGCCACAG	461
Db	301	atatccagatlaaagaaacaagggcttctatcaatgtttcgttcattacataaaggcccaag	360
QY	462	GAATGATTTGGATCCACACATGATGAATTTGCACTGCACTGCTTGCTCAACTTCAGTCAAC	521
Db	361	gactcgtctccatgacacagagatgaattcgcactatcagtgctgtcactactcagtaaac	420
QY	522	CTGAATATGATACCAATTTCTATATTAACAGAAAA--TGTTGATCAATAATTTGACCTGCT	578
Db	421	ctgaataatgttactcttctaataagacaagaatctctgycatacttaatttgccttgc	480
QY	579	CATCTATCAGGTTTACCOCGAACCTTAAGAAGTGTGTTTGGTATGAAACCAAGATT	638
Db	481	catccatacaaggtctaccacgaacccaaggagatgtatttlltggtaaaaccgagaaatc	540
QY	639	CAACTATGAGTATGATGATGATTAATGATGACAAATCTCAGATATATGTCAAGACTGTAACG	698
Db	541	caagactaagatgatalcatgcatgcatgaagaatctcaaaataatgttcaagaaactcata	600
QY	699	ACGTTTCCATCAGCTTGTCGTGTTTCATCTCCGTGATGTACGAGCAATPAGACCATCTCT	758
Db	601	acgcttctcatagcttgcctctccatccagtcctcgaag--caagcaaatgtgacatctctc	657
QY	759	GATTTCTGAAACAGTACAAAGACGGGGTTTTATCTTACCTTCCACTTCTCTATAGA--GCTTG	815
Db	658	ggtctccgaactatgattcaatgaatgaagcttccctccactactaataatagatgcata	717
QY	816	AGGACCTCAGCCTCCCCAGACACAACTTCTTGATTTACAGCTGACTGTCCAA---CAG	872
Db	718	cgaaacccaacccctatgaaacacacactcctctgagatctgcgtctgttgaatgttgg	777
QY	873	TATATTAATATGATGATGATGTTTCTGCTTAATTCATGAAATGGAAGAAAGAGAGCGGC	932
Db	778	tcaatttctgtgtgagtggtgttcttcttaactaagaa---agaaagaagaagcagc	834
QY	933	CTTCGCAACTCTTATTAATGTGGAACAACAACAATGAGAGGAGAGAGACTGACAGACCA	992
Db	835	cttgcgccctcatgtaatctgtgaaaccaacaagaatgtgagaaagaagaatgtgacagacca	894
QY	993	AGAAAAAGAAAAAATTCATATACCTTAAGAAGTCTGATGAAAGCCGAGCTGTTTTAAAA	1052
Db	895	aggaagaaglaagatcacagatgaacgaagaagatctgtctgaagcccggtgt---ttaaca	951
QY	1053	GTTTCGAAGACATCTTCATGACGCAAAAGTGATGATATGTTTTTAAATGAAGATAAGCCC	1112
Db	952	tttcgagaagcagcttcagggcgacaacagtaactacacagttttaataaagataaagtc	1011
QY	1113	A 1113	
Db	1012	A 1012	

such as atopic dermatitis. They can be used in mammals such humans, dogs, cats, cattle, sheep or pets. The products can also be used for detection, diagnosis and drug screening.

Sequence 987 BP; 253 A; 204 C; 215 G; 315 T; 0 other;

Query Match 51.4%; Score 575.2; DB 20; Length 987;
Best Local Similarity 77.8%; Pred. No. 1,6e-162;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

107 ATGATGCCAGTGCATGATGAGGAGTAAATCTCTTGTGATGCTGCTGCTC 166
108 ATGATGCCAGTGCATGATGAGGAGTAAATCTCTTGTGATGCTGCTGCTC 166
109 ATGATGCCAGTGCATGATGAGGAGTAAATCTCTTGTGATGCTGCTGCTC 166
167 TGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 226
168 TGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 226
169 TGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 226
927 TATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 868
928 TATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 868
227 CAATTTGCAACTCTCAAAACCAAGCCTGAGTATGATTTTGGCAGGACGAG 286
228 CAATTTGCAACTCTCAAAACCAAGCCTGAGTATGATTTTGGCAGGACGAG 286
229 CAATTTGCAACTCTCAAAACCAAGCCTGAGTATGATTTTGGCAGGACGAG 286
287 GAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 346
288 GAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 346
807 GATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 748
808 GATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 748
347 AAGTATATGAGGCGCAGCAAGTTTGGATTCGAGAGTGGACCTGAGACTTCA 406
348 AAGTATATGAGGCGCAGCAAGTTTGGATTCGAGAGTGGACCTGAGACTTCA 406
747 AAGTATATGAGGCGCAGCAAGTTTGGATTCGAGAGTGGACCTGAGACTTCA 688
748 AAGTATATGAGGCGCAGCAAGTTTGGATTCGAGAGTGGACCTGAGACTTCA 688
407 CAGATCAAGGACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 466
408 CAGATCAAGGACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 466
687 CAGATCAAGGACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 628
688 CAGATCAAGGACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 628
467 ATTGCGATCCAGCAGATGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTG 526
468 ATTGCGATCCAGCAGATGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTG 526
627 GTTCCCATGACAGCAGATGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTG 568
628 GTTCCCATGACAGCAGATGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTG 568
527 ATAGTACCAATTTTAAATATTAAGCAAAA--TGATGATCAATTTTGGCTG 563
528 ATAGTACCAATTTTAAATATTAAGCAAAA--TGATGATCAATTTTGGCTG 563
567 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 508
568 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 508
584 ATACAGGTTTACCAAGCCTGAGAGTATGATTTTGGTCTAGAACCAAGATTC 643
585 ATACAGGTTTACCAAGCCTGAGAGTATGATTTTGGTCTAGAACCAAGATTC 643
507 ATACAGGTTTACCAAGCCTGAGAGTATGATTTTGGTCTAGAACCAAGATTC 448
644 ATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 703
645 ATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 703
447 ACTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 388
704 TCCATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 763
705 TCCATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 763
387 TCTATCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 331
764 CTGGAAGCTGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 820
765 CTGGAAGCTGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 820
330 CTGCAACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 271
821 CCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 877
822 CCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 877
270 CCCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 211
878 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 937
879 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 937
210 TGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 154
938 AACTCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 997
939 AACTCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 997
153 CCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 94
998 AAGGAAAAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1057
1057 AAGGAAAAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1057

DB 93 AGAGTACGCTACATGATGATGATGATGATGATGATGATGATGATGATG 37
QY 1058 AAGACATCTTATGATGATGATGATGATGATGATGATGATGATGATG 1093
DB 36 AAGACATCTTATGATGATGATGATGATGATGATGATGATGATGATG 1

RESULT 13
T62939
ID T62939 standard; DNA; 764 BP.

AC T62939;

DE 16-JUN-1997 (first entry)

XX Chimeric human/porcine CD86 DNA construct.

XX Xenotransplantation; graft rejection; cell interaction; pig;

XX CD86; monoclonal antibody; chimeric antibody; diagnosis; ss.

XX Chimeric Homo sapiens;

XX Chimeric Sus scrofa.

XX Key Location/Qualifiers

XX CDS /tag- a

XX sig_peptide 7..81

XX mat_peptide 82..756

XX W09711971-A1.

XX 03-APR-1997.

XX 27-SEP-1996; 96WO-US1575.

XX 26-SEP-1996; 96US-0004489.

XX 28-SEP-1995; 95US-0004489.

XX (ALEX-) ALEXION PHARM INC.

XX Evans MJ, Matlis LA, Mueller EE, Mueller JP, Rollins S;

XX Rother RP;

XX WPI: 1997-212855/19.

XX P-PSDB: W14944.

XX Antibodies binding to porcine but not human cell interaction

XX proteins - useful to treat and assay for rejection of xenografted

XX porcine organs, tissues or cells

XX Disclosure; Page 69-70; 105pp; English.

XX A DNA construct (T62939) codes for a chimeric human/porcine

XX CD86 (B7-2) cell adhesion molecule. RT-PCR was used to amplify

XX an internal segment of the porcine CD86 gene from RNA isolated

XX from 11polysaccharide-stimulated porcine peripheral blood

XX lymphocytes. A second PCR fragment encoding a truncated N-terminus

XX was prepd. by 5'RACE PCR. The partial gene fragment was fused to

XX the C-terminal 49 amino acids of the human CD86 IgC domain by

XX overlapping PCR. The 3' primer included 15 nucleotides encoding a

XX histidine tag. Antibodies to porcine CD86 protein are useful for

XX diagnosing human rejection of porcine xenotransplants and for

XX improving xenotransplantation of porcine cells, tissues and organs

XX into human recipients.

XX Sequence 764 BP; 218 A; 197 C; 148 G; 201 T; 0 other;

Query Match 50.6%; Score 566.4; DB 18; Length 764;

us-09-206-132-1.rng

67
83

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•
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/

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 5, 2000, 04:34:36 ; Search time 818.59 Seconds
(without alignments)
8459.355 Million cell updates/sec

Title: US-09-206-132-1
Perfect score: 1120
Sequence: 1 CACAGGAGTGAAGCTTGGCT.....AGAGTAAAGCCCAAAAAA 1120

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
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113: gb_gss14:*
114: gb_gss15:*
115: gb_gss16:*
116: gb_gss17:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID
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1	400.8	35.8	496	22	AW516826	AW516826 xq04h01.x
2	299.6	26.8	448	1	AA056906	AA056906 EST224R.P
C 3	258.4	23.1	570	8	AI093604	AI093604 On82B09.s
C 4	224.2	20.0	504	7	AA946810	AA946810 oq43c01.s
C 5	178	15.9	512	1	AA056905	AA056905 EST224F.P
C 6	172.2	15.4	480	12	AI750143	AI750143 at27h10.x
C 7	163.2	14.6	257	22	AMA27922	AMA27922 64549.MAR
8	134.2	12.0	176	15	AAU076753	AU076753
9	134.2	12.0	176	15	AAU076753	AU076753
C 10	119.8	10.6	380	21	AW260551	AW260551 um83B03.y
C 11	109.8	9.8	391	12	AI632116	AI632116 t8s8B01.x
C 12	104.8	9.4	378	7	AA973397	AA973397 oq44A04.s
C 13	72.4	6.5	450	108	AAQ18422	AAQ18422 HS_5516.E
C 14	48.6	4.3	827	121	CNS000B3	AA064583 drosophila1
C 15	45.4	4.1	1101	121	CNS000B28	AA074533 drosophila1
C 16	43.6	3.9	827	121	CNS000HF	AA073027 drosophila1
C 17	40.8	3.6	61	9	AI184939	AI184939 oK2d810.x
C 18	40	3.6	1101	121	CNS000FU	AA070781 drosophila1
19	40	3.6	567	9	AI228265	AI228265 EST224960
20	39.8	3.6	661	13	BE111752	BE111752 ut-R-B1-1
C 21	39.8	3.6	187	13	AI889413	AI889413 wm9h11.x
C 22	39.6	3.5	975	121	CNS0007Y	AI186438 drosophila1
C 23	39.6	3.5	1101	121	CNS000G2	AA077336 drosophila1
C 24	39.6	3.5	1101	121	CNS000EX	AA072925 drosophila1
C 25	39.4	3.5	909	116	AZ201733	AA077892 drosophila1
C 26	38.8	3.5	624	97	AAQ14440	AZ201733 SP_0052.E
C 27	38.8	3.5	1101	121	CNS0167A	AAQ14440 RPCT-11-1
C 28	38.6	3.5	1201	121	CNS016FX	AA107176 drosophila1
C 29	38.6	3.4	922	121	CNS014FX	AA110695 drosophila1
C 30	38.6	3.4	1102	121	CNS000D4	AI104479 drosophila1
C 31	38.4	3.4	1102	116	AZ188787	AA107675 drosophila1
C 32	38.2	3.4	563	25	AW978061	AZ188787 SP_1012.E
C 33	38.2	3.4	787	121	CNS009LH	AA168484 drosophila1
C 34	38.2	3.4	922	121	CNS015W0	AA058826 drosophila1
C 35	38.2	3.4	997	121	CNS0144P	AA105826 drosophila1
C 36	38.2	3.4	939	121	CNS013PU	AA102493 drosophila1
C 37	38	3.4	983	121	CNS0140J	AA1101868 drosophila1
C 38	38	3.4	482	19	AAW047325	AA110448 drosophila1
C 39	37.8	3.4	536	121	CNS009J2	AAW047325 ut-M-BH1-
C 40	37.8	3.4	781	113	AAQ952743	AA0544325 drosophila1
C 41	37.8	3.4	861	121	CNS0116N	AA095881 drosophila1
C 42	37.8	3.4	903	7	AF122338	AA122338
C 43	37.6	3.4	374	121	CNS000D4Y	AA122338
C 44	37.6	3.4	864	123	CNS0004NY	AA122338
C 45	37.6	3.4	864	123	CNS0004NY	AA122338

RESULT

LOCUS	AM516826	496 bp	mRNA	EST	03-MAR-2000
DEFINITION	xq04r01.x1 Soares.NHCEC cervical tumor Homo sapiens cDNA clone IMAGE:2748913 3' similar to SW:CD86_HUMAN P43081 T LYMPHOCTE ACTIVATION ANTIGEN CD86 PRECURSOR ; mRNA sequence.				
ACCESSION	AM516826				
VERSION	AM516826.1	GI:7154992			
KEYWORDS	EST.				
SOURCE	Homo sapiens human.				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 496)				
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.				
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Robert Strausberg, Ph.D. Tel.: (301) 496-1550 Email: Robert.Strausberg@nih.gov This clone is available royalty-free through LNLN; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone; similarity on wrong strand Seq primer: -400P from Gibco High quality sequence stop: 458. Location/Qualifiers				
FEATURES	Source				
	1..496				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:2748913"				
	/clone_lib="Soares_NHCEC_cervical_tumor"				
	/tissue_type="tumor"				
	/lab_host="DH10B (phage-resistant)"				
	/note="Organ: cervix; Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - Oligo(dt) primer (5'-TGTTACCAATCTGAAGTCGGAGCCGCCGGAAGTTTTTTTTTTTTTTTTTTT 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia); digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. Library is normalized; constructed by Bento Soares and M.Palima Bernaldo."				
BASE COUNT	156 a 102 c 93 g 145 t				
ORIGIN					
Query Match	35.8%; Score 400.8; DB 22; Length 496;				
Best Local Similarity	99.5%; Pred. No. 4.6e-104;				
Matches 402; Conservative	0; Mismatches 2; Indels 0; Gaps 0;				
Gy	715 GTCTGTTCATTCGCCGATGATTACAGCAATATGACAAATCTTCGTATTCGTGAAACTGA	774			
Dd	1 GTCTGTTCATTCGCCGATGATTACAGCAATATGACAAATCTTCGTATTCGTGAAACTGA	60			
Gy	775 CAAGACGCAGCTTTTATCTCACCTTCTCATATAGAGCTTAGAGACCCTCAGCCTCCCC	834			
Dd	61 CAAGACGCAGCTTTTATCTCACCTTCTCATATAGAGCTTAGAGACCCTCAGCCTCCCC	120			
Gy	835 AGACCAATTCCTGGATTACAGCTGTACTTCCACACTTTTATATGTGATGGTTTT	894			
Dd	121 AGACCAATTCCTGGATTACAGCTGTACTTCCACACTTTTATATGTGATGGTTTT	180			
Gy	895 CTGTCTATTTCTATGSAATGAGAAGAGAGAGCGGCTCGCAACTCTTATAAATGTGG	954			
Dd	181 CTGTCTATTTCTATGSAATGAGAAGAGAGAGCGGCTCGCAACTCTTATAAATGTGG	240			
Gy	955 AACCAACACAATGAGAGAGAGAGAGTACAGACCAAAGAAAAGAAAAAATTCATAT	1014			
Dd	241 AACCAACACAATGAGAGAGAGAGAGTACAGACCAAAGAAAAGAAAAAATTCATAT	300			
Gy	1015 ACCTGAAAGATCTGATGAAGCCAGCGGTSTTTTAAAAGTTTGAAGACATCTTCATGCGA	1074			
Dd	301 ACCTGAAAGATCTGATGAAGCCAGCGGTSTTTTAAAAGTTTGAAGACATCTTCATGCGA	360			

QY	1075	CAAAAGCATACATGCTTTTAAATTAAGAGTAAAGCCCAAAA	1118	
Db	361	CAAAAGCATACATGCTTTTAAATTAAGAGTAAAGCCCAATACAA	404	
RESULT	2			
LOCUS	AA056906	448 bp	mRNA	EST 18-SEP-1996
DEFINITION	EST224R Pig spleen lambda gt 11 library (Clontech Cat # PL1006b)			
	Sus scrofa cDNA clone SPL224 reverse similar to U25259 CT1A4			
ACCESSION	AA056906			
VERSION	AA056906.1	GI:1549546		
KEYWORDS	EST.			
SOURCE	pig.			
ORGANISM	Sus scrofa			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
REFERENCE	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.			
AUTHORS	1 (bases 1 to 448)			
TITLE	Tuglie,C.K., Wahls,S. and Schmitz,C.			
JOURNAL	Expressed Sequence Tags from Pig Spleen			
COMMENT	Unpublished (1996)			
	Contact: Tuglie CK			
	Molecular Genetics Laboratory, Department of Animal Science			
	Iowa State University			
	201 Kildee Hall, Ames, IA 50011-3150, USA			
	Tel: 5152944252			
	Fax: 5152942401			
	Email: cktuglie@iastate.edu			
	PCR Primers			
	FORWARD: TGGCGAGACTCTCTG			
	BACKWARD: GACCGGCGCTCAGCT			
	Insert Length: 950 Std Error: 50.00			
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FEATURES				
source	Location/Qualifiers			
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	/db_xref="taxon:9623"			
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	# PL1006b)"			
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	/note="Oligo (dfr) primed"			
BASE COUNT	126 a 116 c 89 g 116 t	1 others		
ORIGIN				
Query Match	26.8%; Score 299.6; DB 1; Length 448;			
Best Local Similarity	80.8%; Pred. No. 4.5e-75;			
Matches 361; Conservative	0; Mismatches 85; Indels 1; Gaps 1			
QY	143	CTCTTTGTGATGCGCTTCCTGCTCTGCTGCTG-CTCCTCTGAGATTCAGCTTATTT	201	
Db	1	CTCTGTGGGATGCTCTCTCGCTCTGTGGCTGCTCTCTTGNAAAAGTCAGCCATATTT	60	
QY	202	CAATGAGACTGCGAGCTCGCATGCCAAATTTGCAACTCTCAACCAACCAAGCCTGATGA	261	
Db	61	CAATGAGACTGCGAGAACTCGGTCCTTTTACAACTCGCAGAACCTAAGCCTGATGA	120	
QY	262	GCTAGTGTATTTTGGCAGACAGCAAGAACTGTTGATGAGGTATCTTAGGCAC	321	
Db	121	GTGGTGTATTTTGGGAGAGACCAAGATACCTGCTCTACAGCTATACGAGGCA	180	
QY	322	AGAGAAATTTGACAGTGTTCATTCACAGTATATGAGGCGGACAAAGTTTGATTCGAG	381	
Db	181	AGAGAAACCTCATATATTTTATTCAGATATATGAGGCGGACAAAGCTTTTACCAAGG	240	
QY	382	TTGAGACCTGAGACTTCATCATCTTCAGATCAAGAGCAAGGCTTTGATCAATGTATCAT	441	
Db	241	CTGAGACCTGAGACTTCACAAAGCTTCAAAATCAAGAGCAAGGCTCATATCAATGTTCAT	300	
QY	442	CCATTCACAAAAGCCACAGAGATGATTCGCATCCACACATGATGAATTCGAACTGTAGT	501	

DB	LOCUS	DEFINITION	ACCESSION	VERSION	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	Source
301	CCATCATTAAGGGCCGCGATGAGCTTCTTCCATCCACGAGATGAGTTCGACCTATACAT												
502	GGTTGGCTAACTTCAGTCAACCTGGAATTAAGTACCAATTTCTTAATATATACAGAAATGTGA												
361	GGTTGGTAACTTCAGTCAACCTGGAATTAAGTACCAATTTCTTAATATATACAGAAATGTGT												
562	CATAAATTGACCTGCTCATCTATACAA												
421	CATAAATTGACCTGCTCATCTATACAA												
RESULT 3													
AI093604	570 bp	EST	10-NOV-1998										
LOCUS	AI093604	570 bp	EST	10-NOV-1998									
DEFINITION	o082p09.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone												
IMAGE:1634297 3'	similar to SW:CD6_HUMAN P42081 T LYMPHOCTE												
ACTIVATION ANTIGEN CD86	PRECURSOR ; mRNA sequence.												
AI093604													
AI093604.1	GI:3432580												
EST.													
human.													
Homo sapiens													
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;													
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.													
1 (bases 1 to 570)													
NCI-CGAP http://www.ncbi.nlm.nih.gov/cgi/gap													
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),													
Tumor Gene Index													
Unpublished (1997)													
Contact: Robert Strausberg, Ph.D.													
Mel: (301) 496-1550													
Email: Robert.Strausberg@nih.gov													
This clone is available royalty-free through LNL; contact the													
IMAGE Consortium (info@image.lnl.gov) for further information.													
Insert Length: 801 Std Error: 0.00													
Seq primer: -40ml3 fwd. ET from Amersham													
High quality sequence stop: 400.													
Location/Qualifiers													
1..570													
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/clone_id="Soares_NSF_F8_9W_OT_PA_P_S1"													
/lab_host="DH10B"													
/note="Organ: pooled. Vector: pT7/3D-Pac (pharmacia) with													
a modified polylinker. Site_1: Not I; Site_2: Eco RI;													
Equal amounts of plasmid DNA from five normalized													
libraries were mixed, and ss circles were made in vitro.													
Following HAP purification, this DNA was used as tracer in													
a subtractive hybridization reaction. The driver was													
PCR-amplified cDNAs from pools of 5,000 clones made from													
the same 5 libraries. The pools consisted of the following													
1:													
309384-310919, 323208-325895 Soares NB2HP pool 1:													
145032-147335, 147720-148103, 148872-149255, 15002 -													
150407, 151176-152327 Soares NB2HP8-9W pool 1:													
758980-760583, 772104-774407 Soares NBHPA pool													

Qy	875	ATTATATGTGATGTTTCTGTCTAATCTATGGAATGGAAAGAAAGACGGCT	934
Db	510	AFCATGTGTATGGTCTCTGTCTAGTCTATCGAAATCGGAAGAAAGAGCGGCT	451
Qy	935	CGCAATCTTTAAATGTGGAACCAACAATGAGAGGAAAGAGTGAACAGACAG	994
Db	450	CGCACTCTTATTAATGT - GAACCAACAATGAGAGGAAAGAGTGAACAGACAG	392
Qy	995	AAAAAGAAAAATCCATATACCTGGAAAGATCGATGAAACCCACGGCTTTAAAGT	105
Db	391	AAAAAGAAAAATCCATATACCTGGAAGATCTGATGAAACCCACGGCTTTAAAGT	332
Qy	1055	TGCAATACATCTTCATGGCAAAAAAGTATACATGTTTTTATTAAGATGAAGCCCA	111
Db	331	TGCAATACATCTTCATGGCAAAAAAGTATACATGTTTTTATTAAGATGAAGCCCA	272
Qy	1115	AAAA 1118	
Db	271	ACAA 268	

RESULT	4
C	AA946810/c
LOCUS	
DEFINITION	504 bp mRNA EST 23-JUL-1998 oq4c001.s1 NCI-CGAP_Kid5 Homo sapiens CDNA clone IMAGE:1583088 3
VERSION	similar to SW:CB86.HUMAN P42081 T LYMPHOCYTE ACTIVATION ANTIGEN
KEYWORDS	CD86 PRECURSOR ;; mRNA sequence.
SOURCE	AA946810 GI:3110205
EST.	human.

Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 - Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCI (bases 1 to 504)
 NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strussberg, Ph.D.

FEATURES
source
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution Information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1276 Std Error: 0.00
 Seq primer: -40m13 fwd. Err from: Amersham
 High quality sequence stop: 457.
 Location/Qualifiers
 1..504

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FEATURES
Source
Location/Qualifiers
1..504
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/tissue_type="2, pooled tumors (clear cell type)"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I, oligo(dAT), primer [5' AACTGGAGAGATTTCGCGCCGCCAATATTTTCTTTTCTTTT 3'], double stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT
136 a 94 c 109 g 165 t

```

	Query Match	Score	224.2	DB	7	Length	504
	Best Local Similarity	98.7%	Pred.	1.96-53			
	Matches	226	Conservative	0	Mismatches	33	Indels
							0
							Gaps
							0
Qy	890	GTTCCTGCTATATTCATATGAAATATGAAAGAAAGAGCGCTCCGCACTCTTATAAA	949				
Db	504	GTTCCTGCTATATTCATATGAAATATGAAAGAAAGAGCGCTCCGCACTCTTATAAA	445				
Qy	950	TGTGGAACCAACCATGTGAGAGGAGGAGGTGACAGACAGAGAAAGAGAAAAATC	1009				
Db	444	TGTGGAACCAACCATGTGAGAGGAGGAGGTGACAGACAGAGAAAGAGAAAAATC	385				
Qy	1010	CATATACCTGAAAGATCTATATGAACCCAGCGCTGTTTTAAATGTGAGACATCTCA	1069				
Db	384	CATATACCTGAAAGATCTATATGAACCCAGCGCTGTTTTAAATGTGAGACATCTCA	325				
Qy	1070	TGCGACAAAAGTATACATGTTTTTATTTAATTAAGACTAAAGCCCAAAA	1118				
Db	324	TGCGACAAAAGTATACATGTTTTTATTTAATTAAGACTAAAGCCCAATCA	276				

[illegible]

```

FEATURES
source
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: ektunglee@iastate.edu
PCR Primers
FORWARD: TGCGCAGCAGCTCCTG
BACKWARD: GACCGGCGCTCAGCT
Insert Length: 950 Std Error: 50.00
Seq primer: TGCGCAGCAGCTCCTG.
location/Qualifiers
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/db_xref="taxon:9823"
/clone="SP1224"
/plone.lib="Pig spleen lambda gt 11, library (Clontech Cat
# PI1006b)"
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/dev_stage="adult"
/note="Oligo (GT) primed"
BASE COUNT
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ORIGIN

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				Pred. No. 3.4e-40	
	Matches 352	Conservative 0	Mismatches 144	Indels 30	Gaps 6
QY	593	TACCACGAACCTTAGAGATGAGTGTGGTCTAACACCAAGAAATTCACATATGCGATAT	652		
db	512	TACCAGAACCCGAGGAGTATATGTGGTCTGAATATACGAAGATTCACACCTGCGAT	453		

QY	653	GATGCTATTATAGCGAANAATGTCAGAAATTAATGTGTCAGCAAACTGTACAGACGTTTCCATCAGC	712
Db	452	GATCTCAGATGAGGAATATCCAAATATACATCAC--GGATTTTACATGTATCATTCAGG	394
QY	713	TTGTCTGTTCATTCCTCGATGTTAGGAGCAATATGACATCTTCTGTATTTGGAAACT	772
Db	393	GTGCTCTTCCCATCTCCCG--AGACAAATGTGAGCATNGTCTGTGTCGCAACTT	337
QY	773	GA-----CAAGAGGGGCTTTATCTTCACCTTCTCTATAGAGCTGTGAGAACCT--	823
Db	336	GAGCGAAGCAAGACAGCTGTTTCTTCCCTACCTTGTATATAGTATGCAAAAGCCACCTGTG	277
QY	824	---CAGCTCCCCAGACCAATCTCTGTGATTTACAGCTACTTCCACA--GTTATT	877
Db	276	CACCCCTGTGCCAGACACATCTNTGGATTGCACCTACTTGTAAACAGTGGTGT	217
QY	878	ATATGTGATGTTTCTGTCTTAATTCATATGAGAAATGAGAAAGAAAGAACGCGCTCGC	933
Db	216	GTGTGTGGAGTGTCTCTTGTAACTAAGAGAAAAAGAAAGAAAGACGCTGCGCCC	157
QY	938	AACCTTTTAATGTGGAACCAACATGAGAGGAGAGAGAGATGAAACAGACCACAAA	997
Db	156	TCTATGATGTGTGGAACCATCAATATGAACAGGAAGGGAATGAAACAAACTAAGAC	97
QY	998	AGAGAAAAATCATATACCTGAAAAGATCTGATGAAGCCACAGCTGTTTTTAAAGTTGC	107
Db	96	AG-----AAGTCCATGAAGAGATCTATATATGCCAGTGTGATTTAATATTTTN	48
QY	1058	AAGACATCTCATGCGCAAAAGATATCATGTTTTTAAATAAGA	1103
Db	47	AAGACAGCTTCAGATGACACACAGTACTACAGATTTTTTAAATAAGA	2

Query Match	Best Local Similarity	15.4%	Score 172.2	DB 12	Length 480
Matches 191	Conservative	0	Mismatches 13	Indels 1	Gaps 1
914	TGGAGAGAAACAAGCGGCGCTGCAACTTTTAAATGTGGAACCAACAATGAGAGG	973			
480	TGGAGAGAAACAAGCGGCGCTGCAACTTTTAAATGTGGAACCAACA -AATGGAGAGG	422			
974	GAGAGAGTGAACAGACCAAGAAAAGAAAAATTCATATACCTGAAAGATCTGATGAA	1033			
421	GAGAGAGTGAACAGACCAAGAAAAGAAAAATATATATACCTGAAAGATCTGATGAA	362			
1034	GGCCACGCGTGTTTTAAAGTTCGAAGACATCTTCATGCGACAAAAGTATACATGTTT	1093			
361	GGCCACGCGTGTTTTAAAGTTCGAAGACATCTTCATGCGACAAAAGTATACATGTTT	302			
1094	TAAATTAAGATTAAGCCCAAAAA	1118			
301	TAAATTAAGATTAAGCCCAATACAA	277			

RESULT		6
LOCUS	A1750143/c	
DEFINITION	A1750143 atc27n10.xl Barstead aorta HprtRB6 Homo sapiens cDNA clone IMAGE:236387 J similar to SW:CD86.HUMAN P42081 T LYMPHOCTE ACTIVATION ANTIGEN CD86 PRECURSOR ; mRNA sequence.	EST 22-JUN-1999
ACCESSION	A1750143	
VERSION	A1750143.1	GI:5128407
KEYWORDS	EST .	
SOURCE	human. Homo sapiens	
ORGANISM	Euxariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homniidae; Homo. 1 (bases 1 to 480)	
REFERENCE	Hillier,Y., Allen,M., Bowles,L., Dubouque,T., Geisels,G., Jost,S., Kilman,D., Kueba,T., Lacy,M., Le,N., Lennon,G., Merria,M., Merril,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.	
AUTHORS	WashU-NCI human EST project Unpublished (1997) Contact: Wilson RK	
TITLE	JOURNAL	
COMMENT	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LINL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer:-40bp from Gibco High quality sequence stop: 367.	

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FEATURES
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location/Qualifiers
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/db_xref="taxon:9606"
/clone IMAGE:2356387
/clone_lib="barstead aorta HPLRB6"
/sex="male"
/dev_stage="adult, age 64"
/lab_host="DH10B (phage resistant)"

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DEFINITION	AM427922	257 bp	mRNA	EST	07-JUL-2000
ACCESSION	645519	MARC	3BOV	Bos taurus	CDNA 5', mRNA sequence.
VERSION	AM427922.1				
KEYWORDS	EST.				
SOURCE	EST.				
ORGANISM	cow.				
	Bos taurus				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
	Bovidae; Bovinae; Bos.				
REFERENCE	1 (bases 1 to 257)				
AUTHORS	Smith,T.P.L., Cassis,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,				
	Bennett,G.A., Fahrnerking,S.C., Freking,B.A., Rohrer,G.A., Laegreid,				
	W.W. and Keefe,J.W.				
TITLE	Design and use of four pooled tissue normalized cDNA libraries for				
JOURNAL	EST discovery in cattle				
	unpublished. (2000)				

COMMENT
Contact: smith@fda.usda, AKS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and mimatch 12 options.

FEATURES
source
PCR Primers
FORWARD: AGGAACAGCTATGACCAAT
BACKWARD: GTTTCCGAGTCACGACG
Plate: 30 row: G column: 20
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
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/clone_1lb="MARC 3B0V"
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OY	906	TATGGAATAATCGAAGAAGAAGAACGCCCTCCCAACTCTCTTAATGTGNAACCACACA	: :	965
Dd	468	TTTSSSGNTSCSBQCSCKSKRBAANGNANCNGADNMNNAKSDPMAMAGANANAN	: :	409
OY	966	TGGAGAGGAGAGAGTAGTAACACAGCAAAGAAAAGAAAAATCATATCTGAAAGAT	: :	1025
Dd	408	NNNMGGAANAANAGACMDNDNNNNNCWAAMAANAANAANNNNNNCNMANNAGATYTANN	: :	349
OY	1026	CTGATGAAGCCCAGCCGTCTTTTAAAGTTCGAA	: :	1059
Dd	348	CNNAGNNNNNAANTNNGTTTAAATATCWCMCA	: :	315
RESULT_14				
LOCUS	CNS00H28	1101 bp DNA GSS		03-JUN-1999
DEFINITION	CNS00H28 Drosophila melanogaster genome survey sequence T7 end of BAC: BACR35M08 of RPci-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.			
ACCESSION	AL074533			
VERSION	-AL074533.1 GI:4953909			
KEYWORDS	GSS.			
SOURCE	Fruit fly,			
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Epiphydroidea; Drosofilidae; Drosophilla.			
REFERENCE	1 (bases 1 to 1101)			
AUTHORS	National de Sequençage Direct Submission			
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Séquençage BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)			
COMMENT	Demarcation of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the drosophila melanogaster genome using these BACS. For further information please see http://www.fruitfly.org/The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oseegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPci-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the library pI and Est libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.			
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	/clone-"BACR35M08"			
	/note="end : t7"			
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	- Query Match 4.1%; Score 45.4; DB 121; Length 1101;			
	- Best Local Similarity 42.2%; Pred. No. 0.044; Mismatches 97; Indels 0; Gaps 0.			
MATCHES	89; Conservative 25; Mistakes 97; Indels 0; Gaps 0.			
OY	868	AACAGTATATATATGCTGATGGTTTTCGTCTAATTTCTATGGAATGAGAGAGAAGAA		927
Dd	313	AAATATATTTTTTTCTGTGCTGTGGTACGCTGTTTTGGAAAVMAAWMAASAAAAAAAAA	: : : : : : : : : : : : : : : : : : :	372
OY	928	GCGGCCTCGCACTCTTATTAATGTGGAACCAACACATGTGAGAGGAAGAGAGTAACA		987

[illegible]

Wed Nov 8 16:52:06 2000

us-09-206-132-1.rst

Page 10

[illegible]

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Search completed: November 5, 2000, 16:41:51
Job time: 43635 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 6, 2000, 01:12:43 ; Search time 360.87 seconds
(without alignments)
29,126 Million cell updates/sec

Title: US-09-206-132-2

Perfect score: 1733
Sequence: 1 MDPCCTMGLSLNLFVMAFL.....AQRVFKSKTSCKDSKDTGCF 329

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: SwissProt-39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1733	100.0	329	1	CD86_HUMAN
2	963.5	55.6	330	1	CD86_RABIT
3	743.5	42.9	309	1	CD86_MOUSE
4	244	14.1	306	1	CD80_MOUSE
5	243	14.0	299	1	CD80_RABIT
6	201.5	11.6	288	1	CD80_HUMAN
7	179	10.3	524	1	BUTY_MOUSE
8	167	9.6	526	1	BUTY_HUMAN
9	165.5	9.5	558	1	Y653_HUMAN
10	162	9.3	526	1	BUTY_HUMAN
11	128	7.4	274	1	OX2G_HUMAN
12	128	7.4	278	1	OX2G_RAT
13	124.5	7.2	365	1	CD80_MOUSE
14	124	7.2	569	1	TACT_HUMAN
15	119.5	6.9	646	1	MU18_HUMAN
16	118.5	6.8	365	1	CD86_HUMAN
17	114	6.6	837	1	NCM2_MOUSE
18	109	6.3	348	1	KILO_RAT
19	108.5	6.3	344	1	NTF1_RAT
20	106	6.1	243	1	CD48_HUMAN
21	105	6.1	335	1	SLAM_MOUSE
22	102	5.9	484	1	PAR2_XENLA
23	101.3	5.9	738	1	PAF_BOVIN
24	101	5.8	1274	1	BXF_CLOBO
25	100.5	5.8	337	1	G55A_CHICK
26	99	5.7	564	1	C166_BRARE
27	98.5	5.7	978	1	KFMS_FSVMD
28	97.5	5.6	285	1	FCG2_RAT
29	97.5	5.6	319	1	A33_HUMAN
30	97.5	5.6	978	1	KFMS_RAT
31	97	5.6	315	1	HEMA_VACCT
32	97	5.6	343	1	SLAM_MOUSE
33	96	5.5	246	1	MOC_BOVIN

ALIGNMENTS

RESULT	ID	CD86_HUMAN	STANDARD:	PRT:	329 AA.
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35	95	5.5	417	1	PVR_HUMAN
36	94.5	5.5	583	1	C166_MOUSE
37	94.5	5.5	588	1	C166_CHICK
38	94.5	5.5	811	1	FS22_DROME
39	94.5	5.5	873	1	FS21_DROME
40	94.5	5.5	1900	1	STF4_YEAST
41	94	5.4	490	1	Y032_BORBU
42	94	5.4	964	1	DROL_CBEPV
43	93.5	5.4	245	1	MOC_RAT
44	93.5	5.4	345	1	OPCM_HUMAN
45	93.5	5.4	583	1	C166_HUMAN

CD86_HUMAN	1	CD86_HUMAN	STANDARD:	PRT:	329 AA.
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DT	01-NOV-1995	(Rel. 32, Last sequence update)			
DT	15-JUL-1998	(Rel. 36, Last annotation update)			
DE	T LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2				
DE	ANTIGEN) (CTLA-4 COUNTER-RECEPTOR B7.2) (B70) (FUN-1) (B063).				
GN	CD86 OR CD28LG2.				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
RN	[1]				
RX	SEQUENCE FROM N.A.				
RX	MEDLINE: 94053735.				
RA	Freeman G.J., Gribben J.G., Boussoletis V.A., Ng J.W.,				
RA	Restivo V.A., Jr., Lombard L.A., Gray G.S., Nadler L.M.;				
RT	"Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T				
RT	cell proliferation."				
RL	Science 262:909-911(1993).				
RN	[2]				
RP	SEQUENCE OF 7-329 FROM N.A.				
RX	MEDLINE: 94050123.				
RA	Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H.,				
RA	Nadler L.L., Somoza C.;				
RT	"B70 antigen is a second ligand for CTLA-4 and CD28."				
RL	Nature 366:76-79(1993).				
RN	[3]				
RP	SEQUENCE OF 7-329 FROM N.A.				
RC	TISSUE=FORESKIN.				
RX	MEDLINE: 95331831.				
RA	Jellis C.L., Wang S.S., Rennett P., Borriello F., Sharpe A.H.,				
RA	Green N.R., Gray G.S.;				
RT	"Genomic Organization of the gene coding for the costimulatory human				
RT	B-lymphocyte antigen B7-2 (CD86)."				
RL	Immunogenetics 42:85-89(1995).				
RN	[4]				
RP	CHARACTERIZATION.				
RX	MEDLINE: 95088403.				
RA	Nadler L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,				
RA	Okumura K., Ito D., Azuma M.;				
RT	"CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T				
RT	cell proliferation, cytokine production, and generation of CTL."				
RL	J. Immunol. 154:97-105(1995).				
RN	[5]				
RP	IDENTIFICATION AS CD86.				
RX	MEDLINE: 94348060.				
RA	Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M.,				
RA	Nadler L.M., Wakasa H., Tedder T.F.;				
RT	"The B7-2 (B70) costimulatory molecule expressed by monocytes and				
RT	activated B lymphocytes is the CD86 differentiation antigen."				
RL	Blood 84:1402-1407(1994).				
CC	-1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL				
CC	FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY				
CC	BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY				


```
CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
CC SUCH AS DECIDING BETWEEN IMMUNITY AND ENERGY THAT IS MADE BY T
CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED B LYMPHOCYTES AND
CC MONOCYTES.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.
CC -1- DATABASE: NAME-PROM; NOTE-CD guide CD86 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/PROM/CD/CD86.HTM"
CC
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CC
CC EMBL; L25259; AA058389.1; -
CC EMBL; U04343; AAB03814.1; -
CC EMBL; U17722; AAA86473.1; -
CC EMBL; U17717; AAA86473.1; JOINED.
CC EMBL; U17718; AAA86473.1; JOINED.
CC EMBL; U17719; AAA86473.1; JOINED.
CC EMBL; U17721; AAA86473.1; JOINED.
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CC INTERPRO: IPR000495; -
CC PROSITE: PS00290; IG_MHC; FALSE NEG.
CC Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
CC Receptor.
CC
CC SIGNAL 1 23
CC CHAIN 24 329
CC DOMAIN 24 247
CC TRANSLEM 248 268
CC DOMAIN 269 329
CC DOMAIN 149 225
CC DISULFID 40 110
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CC CARBOHYD 33 33
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CC 121 IRIHOMNSELSVLANFSEPELVPISNTENYVYINLCSSIHGPEPKKMSVLLRTKNSFI 180
CC 121 IRIHOMNSELSVLANFSEPELVPISNTENYVYINLCSSIHGPEPKKMSVLLRTKNSFI 180
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CC 181 EYDGIOMKSDONTVELYDVISLSPFDVTSNMATFCILIEDTKTRLLSSPSIELEDPQ 240
CC
CC 181 EYDGIOMKSDONTVELYDVISLSPFDVTSNMATFCILIEDTKTRLLSSPSIELEDPQ 240
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CC DT 01-NOV-1995 (Rel. 32, Created)
CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
CC DT 01-OCT-1996 (Rel. 34, Last annotation update)
CC DE B LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2
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CC GN CD86.
CC OS Oryctolagus cuniculus (Rabbit).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN-B/J X CHBB; HM;
CC RX MEDLINE; 95369849;
CC RA Isono T., Seto A.;
CC RT "Cloning and sequencing of the rabbit gene encoding T-cell
CC costimulatory molecules."
CC RL Immunogenetics 42:217-220(1995).
CC CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
CC BINDING CD80 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS.
CC SUCH AS DECIDING BETWEEN IMMUNITY AND ENERGY THAT IS MADE BY T
CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.
CC
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CC
CC EMBL; D49842; BAA08642.1; -
CC INTERPRO: IPR000495; -
CC PROSITE: PS00290; IG_MHC; 1.
CC Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
CC Receptor.
CC
CC SIGNAL 1 22
CC CHAIN 23 330
CC DOMAIN 23 247
CC TRANSLEM 248 268
CC DOMAIN 269 329
CC DOMAIN 149 225
CC DISULFID 40 110
CC CARBOHYD 157 218
CC CARBOHYD 33 33
CC CARBOHYD 135 135
CC CARBOHYD 146 146
CC CARBOHYD 154 154
CC CARBOHYD 177 177
CC CARBOHYD 192 192
CC CARBOHYD 213 213
CC CONFLICT 27 27
CC SEQUENCE 330 AA; 37142 MW; 935CD65C57E3EE1 CRC64;
CC
CC Query Match 55.6%; Score 963.5; DB 1; Length 330;
```


CC RECEPTOR.
 CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1 SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL: D49843; BAA08643.1; -
 CC DR INTERPRO: IPR003006; -
 CC DR PFAM: PF00047; 1g; 1.
 CC KW Immunoglobulin domain; T-cell; Glycoprotein; signal; Transmembrane;
 CC Receptor.
 KM SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 299 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
 FT DOMAIN 33 243 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 244 264 POTENTIAL.
 FT DOMAIN 265 299 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 42 122 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 154 222 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 49 115 POTENTIAL.
 FT DISULFID 161 215 POTENTIAL.
 FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 299 AA; 33513 MW; 6744223ECC91DE0 CRC64;

Query Match 14.0%; Score 243; DB 1; Length 299;
 Best Local Similarity 25.8%; Pred. No. 1,1e-11;
 Matches 81; Conservative 65; Mismatches 122; Indels 46; Gaps 14;

3 POSTMTGLSNLFYMAFLSCAPLKIQAIFYENETADLPQCFANSONSLSELVFMDOEN 62
 12 PRLHLKLCILLALAGIHSSGISOYTKSKEMALSCDY-NISIDELARMTRYMKDQO 70
 63 LVINEVYLKGEKFDVSHKYMGRTSPD-SDSWTLRLHNIQIKDKGLYOCIIHKKPTGMI 121
 71 MWLS-IISGVE--VWPEKKNRTFPDIINNLIMLIALRLSDKGTTCVVGKENGSGFR 126
 122 RIHQMSSESVLANFSQPEIYVPSINTENYINLTGSSIHGYDEPK---KMSVLLRTKN 177
 127 REHLTSTVLSIRADFPPPSITDIGHDPNPK-RIRCSASGSGPEPRILAMWDEGEELNAVN 185
 178 STEEYDQIMQSDONVTELYDVISLSVSPDYTSNMTIFCIETETKTRLLSSPSEIELE 237
 186 TTYVD-----QDLDELTVSSELD---NTNNHSIVCLIKYGLS-VSDIIFWMSKR 233
 238 DPOPPDHP-WITAVILPT---VITCVNVECLI--LWKKKKKRRRNSYKCGCTMMER 289
 234 KOEPPIDQLPFVW--IIPVSGALVTLVAVLYCLACRHVAHMKRRTR-----N 278
 290 EESQTKKKREKIH 303
 279 EEYGVTERLSPIYL 292

RESULT 6
 CD80_HUMAN STANDARD; PRT; 288 AA.
 AC P33681;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE T LYMPHOCYTE ACTIVATION ANTIGEN CD80 PRECURSOR (ACTIVATION 87-1
 DE ANTIGEN) (CTLA-4 COUNTER-RECEPTOR B7.1) (B7) (BB1).
 GN CD80 OR CD28LG1 OR CD28LG OR LAB7.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LYMPHOID.
 RA MEDLINE: 90010147.
 RX Freeman G.J., Freedman A.S., Segal J.M., Lee G., Whitman J.F.,
 RA Nadler L.M.;
 RT "B7, a new member of the Ig superfamily with unique expression on
 RT activated and neoplastic B cells.";
 RL J. Immunol. 143:2714-2722(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92307753.
 RA Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C.,
 RA Dupont B.;
 RT "Genomic organization and chromosomal location of the human gene
 RT encoding the B-lymphocyte activation antigen B7.";
 RL Immunogenetics 36:175-181(1992).
 RN [3]
 RP SEQUENCE OF 35-38.
 RX MEDLINE: 91341422.
 RA Freeman G.J., Gray G.S., Gimmi C.D., Lombard D.B., Zhou L.-J.,
 RA White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;
 RT "Structure, expression, and T cell costimulatory activity of the
 RT murine homologue of the human B lymphocyte activation antigen B7.";
 RL J. Exp. Med. 174:625-631(1991).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE: 95088403.
 RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
 RA Okumura K., Ito D., Azuma M.;
 RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T
 RT cell proliferation, cytokine production, and generation of CTL.";
 RL J. Immunol. 154:97-105(1995).
 CC -1 FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
 CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
 CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
 CC RECEPTOR.
 CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1 TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, MACROPHAGES
 CC AND DENDRITIC CELLS.
 CC -1 SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -1 DATABASE: NAME=PROV; NOTE=CD guide CD80 entry;
 CC WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROV/CD/CD80.HTM".
 CC -----
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 CC -----
 CC EMBL: M27533; AAA36045.1; -
 CC EMBL: M83077; AAA58390.1; -
 CC EMBL: M83072; AAA58390.1; JOINED.
 CC EMBL: M83073; AAA58390.1; JOINED.
 CC EMBL: M83074; AAA58390.1; JOINED.
 CC PIR: A45803; A45803.
 CC MIM: 112203; -
 CC DR INTERPRO: IPR003006; -
 CC DR PFAM: PF00047; 1g; 1.
 CC KW Immunoglobulin domain; T-cell; Glycoprotein; signal; Transmembrane;
 CC Receptor.
 KM SIGNAL 1 34
 FT CHAIN 35 288 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
 FT DOMAIN 35 242 EXTRACELLULAR (POTENTIAL).

Query Match	Best Local Similarity	Score	DB 1	Length	288
Matches	78	Conservative	57	Mismatches	109
				Indels	67
				Gaps	17
14	FWAFLLSG----	APLKIQAVFNTALPCQFANSONOSISELY--	VEMODQENLYL	65	
19	FROLVLAGLHFCSCVIVHTRKVEKVALTSC----	GHNVSVEELAQTRIVQKEKKMYL	74		
66	NEVYLCKEKFDSVHSKYMRQTSFD--SDSWTLRLHNLQIDKGLYOOIHHKKRPTGMIRH	124			
75	TMM-----	SGDMIMPEYKRRRTIEDITNNLSIYIALMRPSDETYECVYLKTKDAFKREH	130		
125	QANSELSTVLANSOPEI----	VPISNITEYNYINLTCSIHQYEPKKMSVL-----	LRT	175	
131	LAEVLTSLVADPPTGISIDPELPTSIR-----	RICTSPSGFPEP--HLSWLENGEELNA	184		
176	KNSTIEYDGIOMQSDNVTLEYDVSISLVSFPDYSNMNTICILEETDTRLSSPFE	235			
185	INTVY-----	SQDPRETELAVASKIDF---NMTHNSFPCLIKYGLR--VNOTFWMN	232		
236	LEDPPPPDHT--PW----	ITAVLPVVIICVAVFCLILMKKKKKRPRNSYKCGTMTMRE	290		
233	TTKQHFPEPNLPLPSMAITLISVNGIFVICILCYCF-----	APR-----	CRERR	275	
291	ESEOTKRRREKI	301			
276	RNERL--RRESV	285			
RESULT	7				
BUTY_MOUSE		STANDARD:	PRT:	524	AA.
BUTY_MOUSE					
AC	062556; P97392;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	15-JUL-1998 (Rel. 36, Last sequence update)				
DT	15-JUL-1998 (Rel. 36, Last annotation update)				
DE	BUTYROPHILIN PRECURSOR (BT).				
BTN.					
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=129; TISSUE=MAMMARY GLAND;				
RX	MEDLINE; 97148936.				
RA	Ogg S.L., Komaragiri M.V.S., Mather I.H.;				
RT	"Structural organization and mammary-specific expression of the				
RL	butyrophilin gene."				
RL	Mamm. Genome 7:900-905(1996).				
RN	[2]				
RP	SEQUENCE OF 39-487 FROM N.A.				
RC	TISSUE=MAMMARY GLAND;				
RX	MEDLINE; 96125722.				
RA	Ishii T., Aoki N., Noda A., Adachi T., Nakamura R., Matsuda T.;				
RT	"Carboxy-terminal cytoplasmic domain of mouse butyrophilin				
FT	specifically associates with a 150-kDa protein of mammary epithelial				

```

RT    Cells and milk fat globule membrane.".
CC    Blochim. Biophys. Acta 1245:285-292(1995).
CC    -I- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
CC    MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
CC    ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
CC    MEMBRANE (BY SIMILARITY).
CC    -I- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE.
CC    -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC    -I- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN
CC    ASSOCIATION WITH THE MILK-FAT GLOBULE MEMBRANE DURING LACTATION.
CC    -I- DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING THE LAST HALF OF
CC    PREGNANCY AND IS MAXIMAL DURING LACTATION.
CC    -I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC    ONE V-LIKE DOMAIN, BELONGS TO THE BFM/MOG SUBFAMILY.
CC    -I- SIMILARITY: STRONG, TO THE C-TERMINAL OF RET FINGER PROTEIN (RFP).
CC
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CC    entities requires a license agreement (See http://www.isd-slb.ch/announce/
CC    or send an email to licensel@isd-slb.ch).
CC -----
DR    EMBL; 067065; AAB51034.1; -.
DR    EMBL; S80642; AAB35893.1; -.
DR    MGJ; MGJ:103118; BTN.
DR    INTERPRO: IPRO00107; -.
DR    INTERPRO: IPRO03006; -.
DR    PFAM; PF00622; SPRY; 1.
DR    PFAM; PF00047; Ig; 1.
KW    Transmembrane; glycoprotein; Immunoglobulin domain; Signal.
FT    SIGNAL          1      26
FT     CHAIN         27     524
FT     DOMAIN        27     247
FT     TRANSMEM      248     268
FT     DOMAIN        269     524
FT     CARBOHYD       56     524
FT     CARBOHYD       216     216
FT     CONFLICT       46     46
FT     CONFLICT       117    117
FT     CONFLICT       191    191
FT     CONFLICT       210    210
FT     CONFLICT       363    363
FT     CONFLICT       408    408
FT     CONFLICT       413    414
FT     CONFLICT       420    423
FT     CONFLICT       492    509
SQ    SEQUENCE      524 AA;  58406 MW;  33f4DE2c7704480 CRC64;
Query Match              10.3%; Score 179; DB 1; Length 524;
Best Local Similarity   25.7%; Pred. No. 1.7e-06;
Matches 77; Conservative 50; Mismatches 135; Indels 38; Gaps 14;
QY  20  LSGAPFLAIQ-----AFENETADLPQCFANSONOSISELVFWQDENLVINEVYL-G 71
DB  24  LDSAPFEVTPAQDFEVLAVGSDAELTCGFSPNASSEYMLMFRQTRSTAYL--LYRDG 81
QY  72  KEKFVSYSKMGKGRFSFDSDW----TLRLAHNIQDKKGJLYCGLIHKKRTGMIRRHOM 126
DB  82  QOEOGOQMTEYRGKRIATAGLLDGRATLLIRDVRVSDQGEGRCLEFKDNDFEEAAVY-- 139
QY  127 NSELVIANFSOPAEIVPISNTENVYINTLCSSIHGGPEPKMSVLLRTKNSITIEYGIM 186
DB  140 ---LKVAAVGSDPQT---SMTVQENGEMELFECTSGGWPEQP---VQMRTGREN-LRSTS 190
QY  187 OKSDQNTVELDVDSISLSVPDYTSNMATFCILETDKTRLSSPSFIETLEDPOP-PPDH 245
DB  191 ESKKHNEBGEFTFAVSNMIRDSI-KNNSC-CI---QNILLGCGKEVEISLPAPFVPRLL 244
QY  246 IPWTAVTAPEVLIIVVFCL---ILMMMKKKRRPNRSYKCGTNTMEERESPQRKKRPKH 302

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Db 45 LGSPGLFLFFSLRADTQOEKVRAMVGSDELSCACPEGSFRLNDVYVWQTSKTV 104
QY 66 NEVYLGK-EKPDVSHSKYMGRTSPD-----SDSMTLRLHNIQIDKGLYCIITHKKPTG 119
Db 105 VTHIHPOSSILENDVSRIRNRLALMSPAGMLRGDPSLRLEFNTVPDDEQFHCIV-LSOSLG 163
QY 120 MIRIHOINSELVLANFSOPEIPIVINSITENVYINLTCSSIHGYPEPKMSVLLRTKST 179
Db 164 FOEVLSEVTLHVAANFSVP-VVASPHSPSODELFTCTSTINGTFRP-NVWINKTDSL 221
QY 180 IENDGIMQKSOD-----NTELYVVSISLSVSPDVTSMNITFCILET----- 222
Db 222 LD-----QATQNDTVFIMRMGLXDYVSLRIA---RTSPVNICCIENVLQOMLVGSQ 273
QY 223 -----DKTRLSSPSFIELEDPPPPDHIPW-ITAVIPYITICVMPCILMMKKKKR 275
Db 274 TGNDIGERDKITENPVSTGEKNA-----ATWSTLAVL-----CLLVAVAVAGWVCCR 322

RESULT 10
BUTY_BOVIN STANDARD; PRT; 526 AA.
AC P18892; O18955; O18959;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE BUTYROPHILIN PRECURSOR (BT).
GN BTN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.
RX MEDLINE: 90354441.
RA Jack L.J.W., Mather I.H.;
RT "Cloning and analysis of cDNA encoding bovine butyrophilin, an apical
RT glycoprotein expressed in mammary tissue and secreted in association
RT with the milk-fat globule membrane during lactation."
RL J. Biol. Chem. 265:14481-14486(1990).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-HOLSTEIN-FRIESIAN;
RA Davey H.W., Ogg S.L., Husaini Y., Snell R.G., Korobko I.V.,
RA Mather I.H., Wilkins R.J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RA Seyfert H., Luethen F.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RN CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE: 95293916.
RA Sato T., Takio K., Kobata A., Greenwalt D.E., Furukawa K.;
RT "Site-specific glycosylation of bovine butyrophilin."
RL J. Biochem. 117:147-157(1995).
RN [5]
RN FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
RN MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
RN ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
RN MEMBRANE.
CC -1- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN
CC ASSOCIATION WITH THE MILK-FAT GLOBULE MEMBRANE DURING LACTATION.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE V-LIKE DOMAIN. BELONGS TO THE BTN/MOG SUBFAMILY.
CC -1- SIMILARITY: STRONG, TO THE C-TERMINAL OF RET FINGER PROTEIN (RFP).
CC -----
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CC -----
DR EMBL: M35551; AAB39766.1; -.
DR EMBL: AF005497; AAB62889.1; -.
DR EMBL: Z93323; CAB07533.1; -.
DR PIR: A37821; A37821.
DR INTERPRO: IPR000107; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00622; SPRY. 1.
DR PFAM: PF00047; Ig; 1.
KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1
FT CHAIN 27
FT DOMAIN 27 526 BUTYROPHILIN.
FT TRANSMEM 243 269 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 270 526 POTENTIAL.
FT CARBOHYD 55 55 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (COMPLEX).
FT CONFLICT 35 35 N-LINKED (GLCNAC. . .) (HYBRID).
FT CONFLICT 230 230 Q -> P (IN REF. 3).
FT CONFLICT 230 230 E -> D (IN REF. 1).
SQ SEQUENCE 526 AA; 59276 MW; A14126802BD19284 CRC64;

Query Match 9.38; Score 162; DB 1; Length 526;
Best Local Similarity 23.08; Pred. No. 3,4e-05;
Matches 80; Conservative 61; Mismatches 155; Indels 52; Gaps 16;

QY 5 CTMGLSNLFYMAVLGSAAPL-----KQAVFNFETADICQFANSONSLSELYVFW 57
Db 8 CIAGCLIFILIQPKLDSAPFDVIGQEPFLAVYGEDAELPCRL--SPNVSAKGMELRW 65
QY 58 QDQENLVLENYL--GKEKFDVSHSKYMGRTSPD-----SMTLRHNIQIDKGLYQ 109
Db 66 FREK--VSPAIVFREGQEOGGEEMAEYRGVSLVEDHIAGSVAIVIQEYKASDDEYR 123
QY 110 CIHHKPTGIRIHOINSELVLANFSOPEIPIVINSITENVYINLTCSSIHGYPEPKM 169
Db 124 CFFRQDENYERAIH-----LKVAALGSDPHI--SMKQESGELQLECTSGWYPERO-- 174
QY 170 SVLLRTKSTIEYDGIQKSODNTELYDVSISSVSFPDVTSMNITFCILETDKTRLS 229
Db 175 -VQRTIRHGE-EFPPSMESNRNPDEGLF--TVRASVIIRSSMKANVSCCI-----RNLLG 226
QY 230 SPSTIELEDPOP-PPDHIPMITAV-LPTVIICVMVFCILIMKK-----KKRPRNSYKCG 283
Db 227 QKEKEVVISIPASFPRLTPMVAVALVILVGLTIGISIFFTWRLYKERSQRNRNEF--- 283
QY 284 TMTMERESQTKKREKIH-----PERSDAQRVAKSKTSKCDKS 325
Db 284 -SSKEKLEELKMKRATLHADVTLDPDTAHPHILEYDESKSVRLDS 330

RESULT 11
OX2G_HUMAN STANDARD; PRT; 274 AA.
AC P41217;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).
GN MOX2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RA McCaughan G.W., Clark M.J., Barclay A.N.;
RX MEDLINE: 87192943.
RT "Characterization of the human homolog of the rat MRC OX-2 membrane

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RT glycoprotein."
RL Immunogenetics 25:329-335(1987).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE IMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE V-LIKE AND ONE C2-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X05323; CAA28943.1; ALT. SEQ.
DR EMBL: X05324; CAA28943.1; JOINED.
DR EMBL: X05325; CAA28943.1; JOINED.
DR EMBL: X05326; CAA28943.1; JOINED.
DR PIR: A47639; A47639.
DR MIM: 155970; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig; 2.
KW Transmembrane; glycoprotein; Neurone; B-cell; T-cell; Antigen;
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 26
FT CHAIN 27 274
FT DOMAIN 27 228
FT TRANSMEM 229 255
FT DOMAIN 256 274
FT DOMAIN 27 137
FT DOMAIN 138 228
FT DISULFID 47 117
FT CARBOHYD 156 210
FT CARBOHYD 99 99
FT CARBOHYD 106 106
FT CARBOHYD 133 133
FT CARBOHYD 177 177
FT CARBOHYD 186 186
FT SEQUENCE 274 AA; 30739 MW; 0A9547B48BD8979C CRC64;

Query Match 7.4%; Score 128; DB 1; Length 274;
Best Local Similarity 21.1%; Pred. No. 0.0058;
Matches 63; Conservative 57; Mismatches 120; Indels 58; Gaps 16;

QY 11 NILEFVMAFLISGAAPLKI-----QAYENETADLPQOFANSQNSLSLSEVFWQDQ--- 60
DB 13 SLVWMAVAVLCITROVOVOTDEREDLY--TTSLSKCSLQNAQ-----EALIVTWQKKAV 66
QY 61 --ENLVV-----NEVYLKEKEFSDVSHSKYMGRTSPDSQSWTLRLHNLQIKDKGLYQCIHH 114
DB 67 SPEPMVTFSENHGVIVQPAVKDKINITOLGQNSTITFW-----NITLEDGCGMCLFN- 120
QY 115 KKPLGMRIRHOMNSLSVLNFSQPEIPIPSNITENVYINLTGSSIHGVEPKKMSYLRL 174
DB 121 --TFGFKI-----SGTRACLTLYVQPIYHNLHNTFC--ARPAP---MYFWK 169
QY 175 TKNSTIEYDGIKMSQDNVTELYDVSISSVSPDYTSNMTIFC-ILE-----TDKTRLLS 229
DB 170 VPRSGIENSVYTLISHRGITSVISI--LHKDKPKNOVGKEVICOVLYLHGTVDKQTVN 226
QY 230 SPFSIELEDQPPPDHLPWITAVLPVYIICVMVFCILMKMKKKRRPNRSYKCGTNTM 287
DB 227 KGYWFS-----VPLLISIVSLVILVILSLIYWK-RHRNODRGELISQGVOKM 273

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DT 20-MAR-1987 (Rel. 04, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (MRC OX-2 ANTIGEN).
GN MOX2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85257428.
RA Clark M.J., Gagnon J., Williams A.F., Barclay A.N.;
RT "MRC OX-2 antigen: a lymphoid/neuronal membrane glycoprotein with a
RT structure like a single immunoglobulin light chain."
RL EMBL J. 4:113-118(1985).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND ON THE SURFACE OF NEURONES, THYMOCYTES,
CC B-CELLS, AND FOLLICULAR DENDRITIC CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE V-LIKE AND ONE C2-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X01785; CAA25925.1; -.
DR PIR: A02114; TDRTOX.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig; 2.
KW Transmembrane; glycoprotein; Neurone; B-cell; T-cell; Antigen;
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 30
FT CHAIN 31 278
FT DOMAIN 31 232
FT TRANSMEM 233 259
FT DOMAIN 260 278
FT DOMAIN 31 141
FT DOMAIN 142 232
FT DISULFID 51 121
FT CARBOHYD 160 214
FT CARBOHYD 95 95
FT CARBOHYD 103 103
FT CARBOHYD 110 110
FT CARBOHYD 157 157
FT CARBOHYD 181 181
FT CARBOHYD 190 190
FT SEQUENCE 278 AA; 31088 MW; B5A72DBE7B3116CD CRC64;

Query Match 7.4%; Score 128; DB 1; Length 278;
Best Local Similarity 22.1%; Pred. No. 0.0059;
Matches 70; Conservative 53; Mismatches 128; Indels 66; Gaps 16;

QY 3 POCMGISNILEFVMAFLISGAAPLKI-----QAYENETADLPQOFANSQNSLSLSEVFW 57
DB 9 PCHLSTYSILMAIAVALSTQAVEVOTDERKLLHTTASLCSIKTQQ-----EPLIVTW 64
QY 58 QDO-----ENLV-----LNEVYLKEKEFSDVSHSKYMGRTSPDSQSWTLRLHNLQIKDKGLY 108
DB 65 QKKKAVGPEPMVYTSKAGVIVQPIYKDKINITEGLMTSTFW-----NITLEDGCGY 119
QY 109 OCTLIHKKPLGMRIRHOMNSLSVLNFSQPEIPIPSNITENVYINLTGSSIHGVEPKK 168
DB 120 MCLF-NMFGSGKY-----SGTRACLTLYVQPIYHNLHNTFC--ARPAP--- 168
QY 169 MSVILKTKNSTIEYDGIKMSQDNVTELYDVSISSVSPDYTSNMTIFCIL-----ETD 223
DB 169 -AISWKGTSGISI-NSTESHSHNGTT--SVTSILRVKDKPKNOVGKEVICOVLYLGNVID 224
QY 224 KTRLLSPFSIELEDQPPPDHLPWITAVLPVYIICVMVFCILMKMKKKRRPNRSYKCG 283

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Db 225 YKQSLDKGFWMS-----VPLLSIYSVLIVLISILY-----KRRRN----- 264

QY 284 TTMERESEGTQKKREK 300

Db 265 --OERGESSOGOMRMK 278

RESULT 13

CDXAR_MOUSE STANDARD; PRT: 365 AA.

AC P97792; 009052; 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR HOMOLOG PRECURSOR (MCAR).

GN CXADR OR CAR.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=LIVER;

RX MEDLINE: 97190109.

RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Kithivas A., Hong J.S., Horvitz M.S., Crowell R.L., Finberg R.W.;

RT "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5."

RL Science 275:1320-1323(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C3H/MAI;

RX MEDLINE: 97250541.

RA Tomko R.P., Xu R., Philipson L.;

RT "MCAR: The human and mouse cellular receptors for subgroup C adenoviruses and group B coxsackieviruses."

RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=LIVER;

RA Bergelson J.M., Kithivas A., Crowell T.L., Finberg R.W.;

RT "The murine CAR homologue (mCAR) is a receptor for coxsackie B viruses and adenoviruses."

RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

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CC EMBL: Y10320; CAA71368.1; -

DR EMBL: U90715; AAC53148.1; -

DR EMBL: Y11929; CAA72679.1; -

DR MGD: MGI:1201679; CXADR.

DR INTERPRO: IPR003006; -

DR PFM: PFM0047; 1g; 2.

KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 19

FT CHAIN 20 365

FT POTENTIAL.

CC COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR

CC HOMOLOG.

CC EXTRACELLULAR (POTENTIAL).

CC POTENTIAL.

CC CYTOPLASMIC (POTENTIAL).

CC IG-LIKE C2-TYPE DOMAIN.

CC IG-LIKE C2-TYPE DOMAIN.

CC BY SIMILARITY.

CC BY SIMILARITY.

FT DISULFID 162 212

FT CARBOHYD 106 106

N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 201 201 N-LINKED (GLCNAC. .) (POTENTIAL)

FT CONFLICT 340 365 VAAPNLSRGAAPVITAPQSDGSLV -> FRIATKIDGIT

FT VV (IN REF. 2 AND 3).

SO SEQUENCE 365 AA; 39947 MW; 5445BA452A34B2A2 CRC64;

Query Match 7.2%; Score 124.5; DB 1; Length 365;

Best Local Similarity 24.6%; Pred. No. 0.015;

Matches 78; Conservative 49; Mismatches 125; Indels 65; Gaps 17;

QY 27 KIQAFNEIADLPQOPANS-QNOSLSLVFWODENLVLPV---YLGKEKDSVHSKY 82

Db 28 RIEKAKGETAYLPCKFKFLSPEDOGPDIDMLISPSDNOIVDQVILYSQDKLYDWPYDYL 87

QY 83 MGRFSPDS-----SWTLRHNIOIKDKGYOCIIHKKRPTQMIRHONSELSLVANFS 137

Db 88 KGRHYFTSNVKGSDASINTNQLSDIGTYCKV--KAPG---VANKKFLITLVKPS 142

QY 138 QPE-IVPISITENVYINLTGSSIHGYPEPKKSVLLRPNSTIEYDGIKQSDQNT-- 194

Db 143 GTRCFVDSGEISGNDP-KIKC-----EPKEGSLPLOPE-----WKLSDSQTMP 185

QY 195 -----ELYDVSISSVSFPPDYSNMTIFCLLENDKTRLLSPFSELEDDPPPHIWI 249

Db 186 TPWLAETSTFVYSKKNASSEYSG--TYSC---TVQNRVSDCMLRL-DVYPPSRAGTI 239

QY 250 T-AVLPTVITCVV---FCLILMKWKKKRPNRSYKSGTNTMERESSEGTQKKREKIHIP 304

Db 240 AGAVIGITLALVILGALFCC-----HRRKREKY-----EKVHHIDREDVPP 284

QY 305 ERSDAQRFKSKTSKTS 321

Db 285 KSRITSTARSTYIGSNHS 301

RESULT 14

TACT_HUMAN STANDARD; PRT: 569 AA.

AC P40200;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE T-CELL SURFACE PROTEIN TACTILE PRECURSOR (CD96 ANTIGEN).

GN CD96.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 92218864.

RA Wang P.L., O'Farrell S., Clayberger C., Krensky A.M.;

RT "Identification and molecular cloning of tactile. A novel human T cell activation antigen that is a member of the Ig gene superfamily."

RL J. Immunol. 148:2600-2608(1992).

CC -1- FUNCTION: MAY BE INVOLVED IN ADHESIVE INTERACTIONS OF ACTIVATED T AND NK CELLS DURING THE LATE PHASE OF THE IMMUNE RESPONSE. MAY FUNCTION AT A TIME AFTER T AND NK CELLS HAVE PENETRATED THE ENDOTHELIUM USING INTEGRINS AND SELECTINS, WHEN THEY ARE ACTIVELY ENGAGING DISEASED CELLS AND MOVING WITHIN AREAS OF INFLAMMATION.

CC -1- SUBUNIT: HOMODIMER, LINKED BY A DISULFIDE BOND.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: EXPRESSED ON NORMAL T CELL LINES AND CLONES, AND SOME TRANSFORMED T CELLS, BUT NO OTHER CULTURED CELL LINES.

CC TESTED. IT IS EXPRESSED AT VERY LOW LEVELS ON ACTIVATED B CELLS.

CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT LOW LEVELS ON PERIPHERAL T CELLS AND IS STRONGLY UP-REGULATED AFTER ACTIVATION, PEAKING 6 TO 9 DAYS AFTER THE ACTIVATING STIMULUS.

CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.

CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

CC -1- DATABASE: NAME=PROM, NOTE=CD guide CD96 entry.

CC WWW-HTTP://WWW.NCBI.NLM.NIH.GOV/PROM/CD/CD96.htm.

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DR EMBL: M88282; AAA36662.1; -
 DR PIR: A46462; A46462.
 DR INTERPRO: IPR003006; -
 DR PIRAM: PF00047; 19; 3.
 KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 569 T-CELL SURFACE PROTEIN TACTILE.
 FT DOMAIN 22 501 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 502 525 POTENTIAL.
 FT DOMAIN 526 569 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 534 486 PRO/SER/THR-RICH.
 FT DOMAIN 538 547 PRO-RICH.
 FT DOMAIN 58 125 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 156 238 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 267 346 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 45 118 PROBABLE.
 FT DISULFID 163 231 PROBABLE.
 FT DISULFID 274 339 PROBABLE.
 FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 569 AA; 63887 MW; DF2F3BEE356F3BF2 CRC64;

Query Match 7.28; Score 124; DB 1; Length 569;
 Best Local Similarity 25.3%; Pred. No. 0.03;
 Matches 63; Conservative 44; Mismatches 96; Indels 46; Gaps 15;

QY 28 IQAYFNTADLPQFANSONOSLSLVFQDQENLVLENYVYGRKRPDSVHSGMGRTS 87
 DB 151 IEIEINOTLEIPC-FOUSSSKISSEFYAMSVEDN-GTQETLISONHLISNTLLADRYK 208
 QY 88 FDSDSWTLRLNLIQIKDG-LYOCIIHKKRPTGMIRIHONSELVLANESQPEI-VPIS 145
 DB 209 LGTD-YELHLSPOIFDGRKFSCHIR---VGNKILRSTTVKV---FAKPEIPIYVE 260
 QY 146 NITENVTI--NLRCSSHGPEPKKMSVLRKNTSI--TYDGI-----QKQDQWTE 196
 DB 261 NNSDVIYVERFRFCTCLKNVP---KANITWFDGSLFHDKEGIVYITNEERKGDGFL 317
 QY 197 YDVISISVSFPRDVTNMTFCI-----LETDK-TRLLSS-----PSI-- 234
 DB 318 KSVLTRHSHKPPASDMLTIWCAALSVPPNKYMNISSEKITFLTSGSEISSTDPPLSYTE 377
 QY 235 ELEDPOPP 243
 DB 378 STLDTPSP 386

RESULT 15
 ID M018_HUMAN STANDARD; PRT; 646 AA.
 AC P43121;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR (MELANOMA-ASSOCIATED ANTIGEN
 DE MUC18) (MELANOMA-ASSOCIATED ANTIGEN A32) (S-ENDO 1 ENDOCELLIAL-
 DE ASSOCIATED ANTIGEN) (CD146 ANTIGEN) (MELANOMA ADHESION MOLECULE).
 GN MAM OR MUC18
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-MELANOMA:
 RX MEDLINE; 90099368.
 RA Leuermann J.M., Riettmueller G., Johnson J.P.:
 RT "MUC18, a marker of tumor progression in human melanoma, shows
 RT sequence similarity to the neural cell adhesion molecules of the
 RT immunoglobulin superfamily.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:9891-9895(1989).
 RN [2]
 RP REVISIONS, SEQUENCE FROM N.A.
 RC TISSUE-MELANOMA:
 RX MEDLINE; 93391384.
 RA Sers C., Kirsch K., Rothbacher U., Riettmueller G., Johnson J.P.:
 RT "Genomic organization of the melanoma-associated glycoprotein MUC18:
 RT implications for the evolution of the immunoglobulin domains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:8514-8518(1993).
 RN [3]
 RP SEQUENCE OF 24-44; 98-112; 135-153; 240-260; 379-389 AND 460-478.
 RX MEDLINE; 94215196.
 RA Shih I.-M., Eleder D.E., Spelcher D., Johnson J.P., Herlyn M.:
 RT "Isolation and functional characterization of the A32 melanoma-
 RT associated antigen.";
 RL Cancer Res. 54:2514-2520(1994).
 RN [4]
 RP SEQUENCE OF 27-40; 98-112 AND 236-260.
 RX MEDLINE; 9616302.
 RA Bardin N., Frances V., Lesaulle G., Horschowski N., George F.,
 RT Sampol J.:
 RT "Identification of the S-Endo 1 endothelial-associated antigen.";
 RL Biochem. Biophys. Res. Commun. 218:210-216(1996).
 RN [5]
 RP FUNCTION.
 RX MEDLINE; 94122526.
 RA Johnson J.P., Rothbacher U., Sers C.:
 RT "The progression associated antigen MUC18: a unique member of the
 RT immunoglobulin supergene family.";
 RL Melanoma Res. 3:337-340(1993).
 CC -I- FUNCTION: COULD BE AN ADHESION MOLECULE ACTIVE IN NEURAL CREST
 CC CELLS DURING EMBRYONIC DEVELOPMENT. ITS EXPRESSION MAY ALLOW
 CC MELANOMA CELLS TO INTERACT WITH CELLULAR ELEMENTS OF THE VASCULAR
 CC SYSTEM THEREBY ENHANCING HEMATOGENOUS TUMOR SPREAD.
 CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -I- TISSUE SPECIFICITY: MAY APPEAR AT THE SURFACE OF NEURAL CREST
 CC CELLS DURING THEIR EMBRYONIC MIGRATION. APPEARS TO BE LIMITED TO
 CC VASCULAR SMOOTH MUSCLE IN NORMAL ADULT TISSUES. ASSOCIATED WITH
 CC TUMOR PROGRESSION AND THE DEVELOPMENT OF METASTASIS IN HUMAN
 CC MALIGNANT MELANOMA. EXPRESSED MOST STRONGLY ON METASTATIC LESIONS
 CC AND ADVANCED PRIMARY TUMORS AND IS ONLY RARELY DETECTED IN BENIGN
 CC MELANOCYTIC NEVI AND THIN PRIMARY MELANOMAS WITH A LOW PROBABILITY
 CC OF METASTASIS.
 CC -I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC 3 C2-LIKE AND 2 V-LIKE DOMAINS.
 CC -I- DATABASE: NAME-PROW; NOTE-CD guide CD146; entry;
 CC WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD146.HTM".
 CC -----
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CC EMBL: M29277: AAA20824.1: -
DR EMBL: M28882: AAA20922.1: -
DR EMBL: X68264: CAA48332.1: -
DR EMBL: X68265: CAA48332.1: JOINED.
DR EMBL: X68266: CAA48332.1: JOINED.
DR EMBL: X68267: CAA48332.1: JOINED.
DR EMBL: X68268: CAA48332.1: JOINED.
DR EMBL: X68270: CAA48332.1: JOINED.
DR EMBL: X68271: CAA48332.1: JOINED.
DR MIM: 155735: -
DR INTERPRO: IPR03006: -
DR PFM: PF00047: 19; 5.
KW Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 23
FT CHAIN 24 646 CELL SURFACE GLYCOPROTEIN MUC18.
FT DOMAIN 24 559 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 560 583 POTENTIAL.
FT DOMAIN 584 646 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 122 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 154 229 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 265 327 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 358 414 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 445 506 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 48 116 PROBABLE.
FT DISULFID 161 223 PROBABLE.
FT DISULFID 272 320 PROBABLE.
FT DISULFID 365 407 PROBABLE.
FT DISULFID 452 499 PROBABLE.
FT CARBOHYD 56 56 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 418 418 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 449 449 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 467 467 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 508 508 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 518 518 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 527 527 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 544 544 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 646 AA; 71793 MW; F0645DAEBOBAEC6 CRC64;
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Query Match 6.9%; Score 119.5; DB 1; Length 646;
Best Local Similarity 22.0%; Pred. No. 0.078;
Matches 76; Conservative 60; Mismatches 138; Indels 71; Gaps 14;

QY 13 LEVMAFLSGAAPLKICAYFNETADLPQAFANSQNSISELVWQDQENLVINEVYLGK 72
DB 325 LDTMISLSEPOELLY-----NYVSDVRSAPAPEROSSSITLTCEASSODLEFQWL-R 379
QY 73 EKFDVSVHSKWKRTSFDSDSWTLRLHNLQIKDKGLYQCIIHKKPTGMIIRIHQNSLSV 132
DB 380 EETDQVLR-----GPIQLHDLKREAGGGRVAVSPSIPGLNR-----TOLVK 424
QY 133 LANFSQPELIVPSN--ITENVYINLQSSIHGYPEPKMSVLLRTKNTIEYDGIMOK- 188
DB 425 LAIFGPPMAKREKRVKEMVNLNLSCEA-SGHPRP---TISWNVGTASQDQDQORY 480
QY 189 -----SOD--NVELYDVVISLSVSPDVTSMNTIFCILETDK 224
DB 481 LSTLNVLVPELLETGVECTASNDLGKNTSILFELVNLFTLPD--SNTTGLSTSTAS 538
QY 225 TRLSPPSIELEDOPPPDHIPITAVLPVILCVWF---CLIMKKKKKKRP-RNS 279
DB 539 PHTRANSTSTERKLEPESRGV-----VIYAVICILVLAVALGAVLYFLTKKGLPCRRS 593
QY 280 YKCGTNTMERESQTKKREKIHIPERSDAQRVFKSKTSQCDK 324
DB 594 GK-----QETLPPSRKTELVEVKSCKLPFEMGLQGSSGDK 631
```


Db 184 DTVAKSSNNVTELYNSISLSFSVPE-ASNVSIFCVLQLESWKLPSPYNDATKPRP 242
 QY 242 PRDHIPITAVL-PTVICVWVFCILMKKKKKRRPNRYKCGTNTMESEEDQKKRK 300
 Db 243 DGDHILMALVWLVLCGMFFTLTK-RKKQKOPSHCECTNKVERKESEQTKERV 301
 QY 301 IHIPERSDEAORVFKSSKTSKCDKSDTCF 329
 Db 302 YHETERSDEAOCV-NISKTSAGDNSTTOF 329

RESULT 2
 002838 PRELIMINARY; PRT; 325 AA.

AC 002838;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE CD86.
 GN Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97047772.
 RA Maher S.E., Karmann K., Min W., Hughes C.C., Pober J.S.,
 RA Botwell A.L.;
 RT "Porcine endothelial CD86 is a major costimulator of xenogeneic human
 RT T cells: cloning, sequencing, and functional expression in human
 RT endothelial cells."
 RL J. Immunol. 157:3838-3844(1996).
 DR EMBL: L76099; AAB61307.1; -
 SQ SEQUENCE 325 AA; 36527 MW; 988BE08137B0597D CRC64;

Query Match 55.0%; Score 953; DB 6; Length 325;
 Best Local Similarity 61.4%; Pred. No. 7, 7e-74;

Matches 202; Conservative 44; Mismatches 73; Indels 10; Gaps 8;

QY 7 MGLSNILFVMAFLISGAAPLKIOAYFNETADLPQFANSQNSISLTVFMDQENLYN 66
 Db 1 MGLSNILFVMAFLISGAAPLKIOAYFNETADLPQFANSQNSISLTVFMDQENLYN 66
 QY 67 EYVLGKRFDSVHSKYMGRTSFDSDMTLRLNMQIKDKGLYOCIIHKKPTGMRIRHQ 126
 Db 61 ELYGQKRPNNVSKYMGRTSFDQATWTLRLHNVOIKDKGSYOCFHHKGPGLVPIHQ 120
 QY 127 NSELVLANFSOPELIVPISNTENVINILGSSIHGYPRPKKSVLLRTKNTIEYDGI 186
 Db 121 SSDLSVLANSOPETINLTHTNSVYNILGSSIOGYPRPKKSVLLRTKNTIEYDGI 180
 QY 187 QKSDONTVELDYVSISSVSPDVTSMNTIFCI-LETKTRILSSPFSIEEDP-OPP- 242
 Db 181 KKSQNTITELYNVSIKSLPIPET-NVSIIVCYLQLEPSKTLFLSPCIDAKPPVQPV 239
 QY 243 PDHITPITAVLP-VIICVWVFCILMKKKKKRRPNRYKCG-TNMESEEDQKKRK 300
 Db 240 PDHILMALVWLVLCGMFFTLTK-RKKQKOPSHCECTNKVERKESEQTKERV 298
 QY 301 IHIPERSDEAORVFKSSKTSKCDKSDTCF 329
 Db 299 VYH-ERSDAQCVNLTAKTSADNSTTDF 325

RESULT 3
 09XSX6 PRELIMINARY; PRT; 329 AA.
 AC 09XSX6;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE C86 ANTIGEN.

GN CD86.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Choi I.-S., Hash S., Winslow B.J., Collisson E.W.;
 RT "Sequence analyses of feline B7 costimulatory molecules."
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF157827; AAD42974.1; -
 SQ SEQUENCE 329 AA; 37481 MW; A10621E3C00A088B CRC64;

Query Match 52.1%; Score 903; DB 6; Length 329;
 Best Local Similarity 58.5%; Pred. No. 1, 5e-69;

Matches 190; Conservative 44; Mismatches 83; Indels 8; Gaps 7;

QY 6 TMGLSNILFVMAFLISGAAPLKIOAYFNETADLPQFANSQNSISLTVFMDQENLYN 65
 Db 7 TMGLSNILFVMAFLISGAAPLKIOAYFNETADLPQFANSQNSISLTVFMDQENLYN 66
 QY 66 NEYVLGKRFDSVHSKYMGRTSFDSDMTLRLNMQIKDKGLYOCIIHKKPTGMRIRHQ 125
 Db 67 YELFRKENPQNVHLKYKRTSPDKDMWTLRLHNVOIKDKGYHGFHKKPKGLVPIHQ 126
 QY 126 NSELVLANFSOPELIVPISNTENV-VINILGSSIHGYPRPKKSVLLRTKNTIEYD 184
 Db 127 MSSDLVLANSOPETITVTSNRTENGINILGSSIOGYPRPKKSVLLRTKNTIEYD 186
 QY 185 IMKSDONTVELDYVSISSVSPDVTSMNTIFCI-LETKTRILSSPFSIEEDP-DPO 241
 Db 187 VMKSSQNNVTELYNSISLFSVPE-AHNVSYFCALKLETEMLSLPFDNDAQPKKDP 245
 QY 242 PRDHIPITAVLP-VIICVWVFCILMKKKKKRRPNRYKCGTNTMESEEDQKKRK 300
 Db 246 EOGHFLMIAVLMVFMVFGWVSFTLTK-RKKQKOPSHCECTNKVERKESEQTKERV 304
 QY 301 IHIPERSDEAORVFKSSKTSKCDK 325
 Db 305 YHETERSDEAOCV-NILKTSAGDN 328

RESULT 4
 09TFL1 PRELIMINARY; PRT; 280 AA.
 AC 09TFL1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE TRUNCATED B7-2 PROTEIN.
 GN CD86.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang S., Sim G.-K.;
 RT "New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
 RT Molecules."
 RL Immunogenetics 50:349-353(1999).
 DR EMBL: AF106827; AAF17298.1; -
 DR INTERPRO: IPR000495; -
 DR PROSITE: PS00290; IG_MHC; UNKNOWN.1
 DR PROSITE: PS00290; IG_MHC; UNKNOWN.1
 SQ SEQUENCE 280 AA; 32265 MW; 3C8B6CA4D826A7F3 CRC64;

Query Match 51.2%; Score 886.5; DB 6; Length 280;
 Best Local Similarity 55.7%; Pred. No. 3, 1e-68;

Matches 182; Conservative 40; Mismatches 54; Indels 51; Gaps 4;

QY 4 OCTMGLSNILFVMAFLISGAAPLKIOAYFNETADLPQFANSQNSISLTVFMDQENLYN 63
 Db 4 RCTMGLSNILFVMAFLISGAAPLKIOAYFNETADLPQFANSQNSISLTVFMDQENLYN 63

[illegible]

SEQ	SEQUENCE	314 AA	302683F36CADEDF4	CRC64
061238	PRELIMINARY;	PRT;	314 AA.	
ID	061238			
AC	061238;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, last sequence update)			
DT	01-NOV-1999 (TREMBLrel. 12, last annotation update)			
DE	T CELL COSTIMULATOR MOLECULE B7-2.			
GN	CD86 OR B7-2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrate; Euteleostomi;			
OC	Mammalia; Rodentia; Sciurognathi; Murinae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRATINE-129;			
RX	MEDLINE; 96094437.			
RA	Bortelle F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;			
RT	Differential expression of alternate mab-2 transcripts.			
RL	J. Immunol. 155:5490-5497(1995).			
DR	EMBL; U39456; AAC52335.1; -			
DR	EMBL; U39460; AAC52335.1; JOINED.			
DR	EMBL; U39461; AAC52335.1; JOINED.			
DR	EMBL; U39462; AAC52335.1; JOINED.			
DR	EMBL; U39463; AAC52335.1; JOINED.			
DR	EMBL; U39464; AAC52335.1; JOINED.			
DR	EMBL; U39465; AAC52335.1; JOINED.			
DR	EMBL; U39466; AAC52335.1; JOINED.			
DR	MED; MG1:101773; Cdbb.			
SO	SEQUENCE	314 AA;	302683F36CADEDF4	CRC64;

Query Match	41.8%;	Score 724.5;	DB 11;	Length 314;
Best Local Similarity	51.2%;	Pred. No. 2.6e-54;		
Matches 155; Conservative	44;	Mismatches 91;	Indels 13;	Gaps 5;

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0Y 5 CTMGUSNLLFYMAFLLSGAAPLKIOAFNFENADLPQGFANSQNSISELYVFMODENLY 64
      |||||:::||||:::||||:::||||:::||||:::||||:::||||:::||||:::
Db 10 CTMGALIAIFUYVLLISDAVSETOAFNGFNGAYLPCPEPTKAOINISISELYVFMODOKLY 69
      |||||:::||||:::||||:::||||:::||||:::||||:::||||:::||||:::
0Y 65 LNEVYLGKEKPEPVSXKYMGRSFDSDSWTLRLNLIOIKDKGLQCIILHHKPPGMRIRH 124
      |||||:::||||:::||||:::||||:::||||:::||||:::||||:::||||:::
Db 70 LYEHLVGEKIDSVNAKLYLGRSEDRNNWTLRLNLVQIKDMGSIIDCFIOKKPPGSIILQ 129
      |||||:::||||:::||||:::||||:::||||:::||||:::||||:::||||:::
0Y 125 QMNSSELYANFOPEIPIPSNITENYVINTJGSSIHGYPEPKMSVLLRTKNSITIEDG 184
      |||||:::||||:::||||:::||||:::||||:::||||:::||||:::||||:::
Db 130 QLTLESLVANSSEPEIKLAQWNVGNSGINTJCSKQHPKPKMYFLI--TNSTNEYGD 187
      |||||:::||||:::||||:::||||:::||||:::||||:::||||:::||||:::
0Y 185 IMQSDQNVNTELYDVISLSLVSFPDYVSNNMIFCLFLEFDKTRLLSPSIFLEDBOPPPD 244
      |||||:::||||:::||||:::||||:::||||:::||||:::||||:::||||:::
Db 188 NMQISDQNVNTELYFSNLSISLSPGQVNMHVYVCLLEPNSKISKPLNTEQDEPSP-- 244
      |||||:::||||:::||||:::||||:::||||:::||||:::||||:::||||:::

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[illegible]

SEQ	RESULT	6	
Q64381			
ID	064381	PRELIMINARY;	PRT; 356 AA.
AC	Q64381;		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)		
DE	B7-2.		
GN	CD86 OR B7-2.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
RN	[1]		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=N.A.		
RA	MEDLINE: 96094437.		
RT	Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;		
RL	"Differential expression of alternate mb7-2 transcripts.";		
RL	J. Immunol. 155:5490-5497(1995).		
DR	EMBL: U39456; AAC52332.1; -		
DR	EMBL: U39392; AAC52333.1; JOINED.		
DR	EMBL: U39457; AAC52333.1; JOINED.		
DR	EMBL: U39461; AAC52333.1; JOINED.		
DR	EMBL: U39462; AAC52333.1; JOINED.		
DR	EMBL: U39463; AAC52333.1; JOINED.		
DR	EMBL: U39464; AAC52333.1; JOINED.		
DR	EMBL: U39465; AAC52333.1; JOINED.		
DR	EMBL: U39466; AAC52333.1; JOINED.		
DR	EMBL: U39467; AAC52332.1; -		
DR	EMBL: U39465; AAC52332.1; JOINED.		
DR	EMBL: U39466; AAC52332.1; JOINED.		
DR	EMBL: U39392; AAC52332.1; JOINED.		
DR	EMBL: U39457; AAC52332.1; JOINED.		
DR	EMBL: U39461; AAC52332.1; JOINED.		
DR	EMBL: U39462; AAC52332.1; JOINED.		
DR	EMBL: U39463; AAC52332.1; JOINED.		
DR	EMBL: U39464; AAC52332.1; JOINED.		
DR	EMBL: U39465; AAC52332.1; JOINED.		
DR	EMBL: U39466; AAC52332.1; JOINED.		
DR	EMBL: U39467; AAC52332.1; JOINED.		
DR	EMBL: U39468; AAC52332.1; JOINED.		
DR	EMBL: U39469; AAC52332.1; JOINED.		
DR	EMBL: U39470; AAC52332.1; JOINED.		
DR	EMBL: U39471; AAC52332.1; JOINED.		
DR	EMBL: U39472; AAC52332.1; JOINED.		
DR	EMBL: U39473; AAC52332.1; JOINED.		
DR	EMBL: U39474; AAC52332.1; JOINED.		
DR	EMBL: U39475; AAC52332.1; JOINED.		
DR	EMBL: U39476; AAC52332.1; JOINED.		
DR	EMBL: U39477; AAC52332.1; JOINED.		
DR	EMBL: U39478; AAC52332.1; JOINED.		
DR	EMBL: U39479; AAC52332.1; JOINED.		
DR	EMBL: U39480; AAC52332.1; JOINED.		
DR	EMBL: U39481; AAC52332.1; JOINED.		
DR	EMBL: U39482; AAC52332.1; JOINED.		
DR	EMBL: U39483; AAC52332.1; JOINED.		
DR	EMBL: U39484; AAC52332.1; JOINED.		
DR	EMBL: U39485; AAC52332.1; JOINED.		
DR	EMBL: U39486; AAC52332.1; JOINED.		
DR	EMBL: U39487; AAC52332.1; JOINED.		
DR	EMBL: U39488; AAC52332.1; JOINED.		
DR	EMBL: U39489; AAC52332.1; JOINED.		
DR	EMBL: U39490; AAC52332.1; JOINED.		
DR	EMBL: U39491; AAC52332.1; JOINED.		
DR	EMBL: U39492; AAC52332.1; JOINED.		
DR	EMBL: U39493; AAC52332.1; JOINED.		
DR	EMBL: U39494; AAC52332.1; JOINED.		
DR	EMBL: U39495; AAC52332.1; JOINED.		
DR	EMBL: U39496; AAC52332.1; JOINED.		
DR	EMBL: U39497; AAC52332.1; JOINED.		
DR	EMBL: U39498; AAC52332.1; JOINED.		
DR	EMBL: U39499; AAC52332.1; JOINED.		
DR	EMBL: U39500; AAC52332.1; JOINED.		
DR	EMBL: U39501; AAC52332.1; JOINED.		
DR	EMBL: U39502; AAC52332.1; JOINED.		
DR	EMBL: U39503; AAC52332.1; JOINED.		
DR	EMBL: U39504; AAC52332.1; JOINED.		
DR	EMBL: U39505; AAC52332.1; JOINED.		
DR	EMBL: U39506; AAC52332.1; JOINED.		
DR	EMBL: U39507; AAC52332.1; JOINED.		
DR	EMBL: U39508; AAC52332.1; JOINED.		
DR	EMBL: U39509; AAC52332.1; JOINED.		
DR	EMBL: U39510; AAC52332.1; JOINED.		
DR	EMBL: U39511; AAC52332.1; JOINED.		
DR	EMBL: U39512; AAC52332.1; JOINED.		
DR	EMBL: U39513; AAC52332.1; JOINED.		
DR	EMBL: U39514; AAC52332.1; JOINED.		
DR	EMBL: U39515; AAC52332.1; JOINED.		
DR	EMBL: U39516; AAC52332.1; JOINED.		
DR	EMBL: U39517; AAC52332.1; JOINED.		
DR	EMBL: U39518; AAC52332.1; JOINED.		
DR	EMBL: U39519; AAC52332.1; JOINED.		
DR</			

Query Match	41.3%;	Score 715.5;	DB 11;	Length 356;
Best Local Similarity	51.0%;	Pred. No. 1.8e-53;		
Matches 154;	Conservative 44;	Mismatches 91;	Indels 13;	Gaps 5;

[illegible]

QY 304 PE 305
DB 342 KE 343

RESULT 7

035531 PRELIMINARY; PRT; 313 AA.
AC 035531.
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE MEMBRANE GLYCOPROTEIN PRECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR LEWIS (LEW/CRJ); TISSUE-LYMPHOMA;
RX MEDLINE; 97380318.
RA Maeda K., Sato T., Azuma M., Yagita H., Okumura K.;
RT "Characterization of rat CD80 and CD86 by molecular cloning and mab."
RL Int. Immunol. 9:993-1000(1997).
DR EMBL; D50558; BAA23470.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; 19; 1.
KW Signal; Membrane.
FT CHAIN 30 313 POTENTIAL.
FT CD28 AND CTLA4 LIGAND.
SQ SEQUENCE 313 AA; 35573 MW; 3106246B8901B5D5 CRC64;

Query Match 40.5%; Score 702.5; DB 11; Length 313;
Best Local Similarity 55.0%; Pred. No. 2e-52;
Matches 148; Conservative 33; Mismatches 83; Indels 5; Gaps 3;

QY 5 CTMGSLILFYVAFLLSGAPLKIQAAYFNETADLPQFANSQNSLSELYVFWQDENVL 64
DB 10 CTMYGILFSLVAYLLSAPVAVKQAFVNSAYLPCPFTKAQNSPELAVFWQDKKSV 69
QY 65 LNEYVLGKEKDSVSKMGRTSPDSWTLRLNLDIKKGLKQCLHHKKTGMIRH 124
DB 70 LYEHVLGAEKLDVNAKYLGRFSFDRNQALRLHNVQIKDTGYDCTIQKRTGSIILQ 129
QY 125 QMNSLSVLANFSOPELPIISNTENYINLTCSHIGYPEPKMSVLTRTKSTIEYDG 184
DB 130 QMETELSIANFSEPELEAQNENRNGINLTCSKQGYKPKPMYFLI--TSTNEYGD 187
QY 165 IMQKQDQNTVELYDVYISLSVSPDYVSNMTIFCILETDKTRLLSFSFIELEDPPQPP 244
DB 188 NMQISQDQNTVELYDVYISLSVSPDYVSNMTIFCILETDKTRLLSFSFIELEDPPQPP--PD 245
QY 245 HIPMTAVLPVVICVWFCLILMKMKKK 273
DB 246 RKTWQIAGPSSLCCFLVYVKKKK 273

RESULT 8

062810 PRELIMINARY; PRT; 149 AA.
AC 062810.
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE 01-AUG-1998 (TREMblrel. 07, Last annotation update)
DE B7-2 (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LUNG;
RA Goodman R.E., Pastoriza L., Pak J.J., Toews G.B.;

RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U31330; AAA74282.1; -.
FT NON_TER 1
FT NON_TER 149 149
SQ SEQUENCE 149 AA; 17153 MW; A649D99DFEC42F11 CRC64;

Query Match 26.1%; Score 453; DB 11; Length 149;
Best Local Similarity 62.4%; Pred. No. 1.7e-31;
Matches 93; Conservative 15; Mismatches 39; Indels 2; Gaps 1;

QY 49 SLSELYVFWQDENVLNEYLGKEKDSVSKMGRTSPDSWTLRLNLDIKKGLY 108
DB 2 SLSELYVFWQDKKSVLYEHYLGAEKLDVNAKYLGRFSFDRNQALRLHNVQIKDTGYL 61
QY 109 QCIHHKPKGMIRHQMNSLSVLANFSOPELPIISNTENYINLTCSHIGYPEPK 168
DB 62 DCFIQKPTGISILQWETELSIANFSEPELEAQNENRNGINLTCSKQGYKPK 121
QY 169 MSVLTRTKSTIEYDGIMQKQDNTLEY 197
DB 122 MYFLI--TSTNEYGDNMQISQDNTLEY 148

RESULT 9

09R129 PRELIMINARY; PRT; 306 AA.
AC 09R129.
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMblrel. 14, Last annotation update)
DE B LYMHOCYTE ACTIVATION ANTIGEN CD80 PRECURSOR.
GN CD80.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/J; TISSUE-SPLEEN;
RA Ma R.Z., Teuscher C.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065893; AAD25876.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; 19; 2.
SQ SEQUENCE 306 AA; 34531 MW; 1DB9EE3B6C1921F2 CRC64;

Query Match 14.0%; Score 243; DB 11; Length 306;
Best Local Similarity 27.9%; Pred. No. 4e-13;
Matches 89; Conservative 57; Mismatches 121; Indels 52; Gaps 16;

QY 12 ILFYVAFLLSGAPLKIQAAYFNETAD--LPQFANSQNSLSELYVFWQDENVLNEY 68
DB 23 LLFYVILRLSQVSDVDEQSKSVKDKVLLPCRY--NSPHEDESEDRITQKDKVYLS-V 80
QY 69 YLGKEKDSVSKMGRTSPDSWTLRLNLDIKKGLKQCLHHKKTGMIRH-HQMN 127
DB 81 TAGKLR--VPEYKNTLTDNTYISLILGLVLSDRGTSCVY--OKKRGYEVKHAL 136
QY 128 SELSVLANFSOPELPIISNTENYINLTCSHIGYPEPKMSVLT--LRTKSTIEY 182
DB 137 VKLSIKADESTPNITSEGNPSAGTK--RITCFASGCPKP--RESWLENRELPGIMTTI-- 192
QY 183 DGMQKQDQNTVELYDVYISLSVSPDYVSNMTIFCILETDKTRLLSFSFIELEDPPQPP 242
DB 193 -----SQDPESELYTSSQLDPR--NTRNHTIKCLIRYGAH--VSEDFWE--KPPDP 241
QY 243 PDHPIWTT-----AVLPVVICVWFCLILMKMKKKRRPNYSYKCGTNTRESESEOT 295
DB 242 PDSKNTLVLGAGGAVITVIVITIKKCC-----KHSKCF-----RNEASRE 286
QY 296 KRREKIHPESEDAQRYF 314

DB 287 TNNSLTFGEPEALAEQTVF 305

RESULT 10

ID 046405 PRELIMINARY; PRT; 296 AA.

AC 046405; 046405;

DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

DE CD80 ANTISEN PRECURSOR (FRAGMENT).

OS Bos laurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;

OC Bovidae; Bovinae; Bos.

RN [1]

RP SEQUENCE FROM N.A.

RA Parsons K.R., Howard C.,

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; Y09950; CAA71081.1; -.

DR INTERPRO; IPR003006; -.

DR PFAM; PF00047; 19; 2.

KW Signal.

FT NON_TER

SQ SEQUENCE

296 AA; 33618 MM; 7ADB1FB5F532EF5 CRC64;

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DR INTERPRO: IPR003006; -.

DR PFAM: PF00047; 19; 2.

SQ SEQUENCE 292 AA; 33482 MM; 6F117E7852B7950F CRC64;

Query Match 12.9%; Score 224; DB 6; Length 292;

Best Local Similarity 27.7%; Pred. No. 1.6e-11;

Matches 78; Conservative 61; Mismatches 103; Indels 40; Gaps 17;

DB 12 ILFVAFLLSGAAPLKIAQAFNETADLPQAFANSONSLSLVVFNQDQENLYLNEVYL 71

DB 24 MLASLFFGSGI--IQVKKVEEVAALVSCDY--NSTELEIRIYWKQDEMYL-AVMSG 79

DB 72 KEKFDVSYSKYMGRTSPD--SDSWTLRLNLQIKDKGLYOCIIHKKRPTGMIRIHOMNS-E 129

DB 80 KYQ--VMPKYNKRTFTVDNDHNSIVIALRLSDNGKATCI--QKIEGSKYKHLTSVM 135

DB 130 LSVLANFSOPELVIPISNTENYINLTGSSIHGIPERKMSVL-----LTKNSTIYDG 184

DB 136 LTVRADFPVPSITDIGNPSHNIR-RIMCLTSGGPPKP-HLSWLENEBELNAINTV--- 189

DB 185 IMQKSDNVTLEYDVISLSVSPDVTSMNTIFCILETDKTRLSSPFILEDPPPPD 244

DB 190 ----SQDETELXTISSLEDF---NMTNHSFLCLVYKGNL-LVSQIFNMQKSPQPSNN 241

DB 245 HTPWITAVLPVITCVMPF-----CLT---LKKKKKKRPR 277

DB 242 QL-WI-ILISVYSGIIVITALTLCIVHRPAPARWOREMR 281

DB 055202 PRELIMINARY; PRT; 321 AA.

AC 055202; 055202;

DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

DE CD80.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RN [1]

RP SEQUENCE FROM N.A.

RA Sato T., Azuma M., Yagita H., Okumura K.;

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; U88622; AAC02262.1; -.

DR INTERPRO: IPR003006; -.

DR PFAM: PF00047; 19; 2.

SQ SEQUENCE 321 AA; 36297 MM; 07E5B56E588ED6AF CRC64;

321

36297

07E5B56E588ED6AF

CRC64;

321

36297

07E5B56E588ED6AF

CRC64;

321

36297

07E5B56E588ED6AF

CRC64;

321

36297

07E5B56E588ED6AF

CRC64;

321

36297

07E5B56E588ED6AF

CRC64;

321

36297

07E5B56E588ED6AF

CRC64;

321

36297

07E5B56E588ED6AF

CRC64;

321

```

QY      185 IMKSDONTALTYDVISLSISLSPFPMVSNMTICILETOKTRLLSPSIELEDPDPP 244
           ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      195 -----SQDPSESLYTTSQLDF-----NTYYDHRIQCIFIEYGAAH-VGQNFTWE-KPEDPDP 245
QY      245 H---IF--W-----ITAVLPVLIIICWMVCLIMKKMKKKRRNSYCKGT 285
           ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      246 EKOTITFPNAGSGDAKAKAIIIFIATIVIAVAIAIATIIIFCIIV-FRRCGFERRN----- 296
QY      285 NIMERESEECQTK 297
           | :| :|
Db      299 -----EASRETNK 306

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RESULT	13		
062624			
ID	062624	PRELIMINARY;	PR: 321 AA.
AC	062624;		
DT	01-NOV-1996 (TReMBLrel. 01.	Created)	
DT	01-NOV-1996 (TReMBLrel. 01.	Last sequence update)	
DT	01-MAY-2000 (TReMBLrel. 13.	Last annotation update)	
DE	B7-1.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=SPLEEN;		
RX	MEDLINE; 95252184.		
RA	Cloning T. A., Liu M., Christensen P. J., Fak J. J., Turka L. A.;		
RT	"Cloning the rat homolog of the CD28/CTLA-4-ligand B7-1: structural		
RT	and functional analysis."		
RL	Int. Immunol. 7:171-178(1995).		
DR	EMBL; U05593; AAA80154.1; ..		
DR	INTERPRO; IPR003006; ..		
DR	PRIM; PF00047; 19; 2.		
QQ	SEQUENCE 321 AA; 36252 MM; EBD36B3BD31E1456 CRC64;		

Query Match	12.8%	Score 222;	DB 11;	Length 321;
Best Local Similarity	25.5%;	Pred. No. 2.6e-11;		
Matches	83;	Conservative	59;	Mismatches 116;
			Indels	68;
			Gaps	17;

```

0Y 7 MGJSLNLFVMAJLLSGAPLKTQ-----YFNFTALPQGF-NSONOSLSBYW 57
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
14 LGPRLRTHLEFVLLVGLDSSIGYQVSKSVREKALLSCDQKFCSEOSIHR--TW 71
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

0Y 58 QDQENLVLENYVLGKEKFDVSHKXMGRTSFD--SDWTLRLNLQIKDKGLYQCIHHK 116
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 72 QKDHKKLVSVI-----SGVEPWPKYKKNRTVYDIANNSESLGLILSRGYTCVOYE 127
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

0Y 117 PTGMIRIHOHNSLSVLANFSGPEIIVPISNTENYVINTLGSIHGYEPKMSVL---- 172
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 GGSYVVKHLLTYELSVRADPFLPMITEGNPSADIK-RITCASGSPKRP-RLSLWENGR 185
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

0Y 173 -LRTKSTIEYGIQKQSDQNVTELDYVSISSLSVSPDYVTSNMATIPCLLEFDKTRLSSP 231
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 186 ELWGIWTT-----SQDESELYTISQLDF--NATYHFIIDCFIEYGDAH-VSON 233
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

0Y 232 FSIELDDPPPPDH--LP-W-----ITAVLPVYICWYFGLMKMK 271
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 234 FT-WKRPEDPPDEKQYLPFMAAGPDVAKAIIIFAIIVAVIAAIIIFICTV-KFR 291
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

0Y 272 KKKRPANSTKCGTNTMEDESQTKK 297
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 292 KCFRRN-----EASRETNK 306
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 14	
035187	
ID 035187	PRELIMINARY;
AC 035187;	PRG; 321 AA.
DT 01-JAN-1998	(TRENDArel. 05, Created)
DT 01-JAN-1998	(TRENDArel. 05, Last sequence update)

DT 01-MAY-2000 (Tremblere, 13, last annotation update)
DE B7.1.
GN B7.1.
OS *Rattus norvegicus* (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISCHER.
RC Wildgeen B., Visse E., Sjogren H.O.,
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF010465; AAB66351.1; -
DR INTERPRO: IPR003006; -
DR Pfam: PF00047; 1q; 2
SQ SEQUENCE 321 AA; 36351 MW; 071C6007FBBD1E60 CRC64;

Query Match	12.7%	Score 220;	Db 11;	Length 321;
Best Local Similarity	25.9%	Pred. No. 3,9e-11;		
Matches	81;	Conservative	57;	Mismatches 115; Indels 60; Gaps 16;
Qy	12	ILPYMAFLISGAAPKIQIAFNETDLEPCQRA-NSQNSQSELYVFWQDQENLYLAENEYL	70	
Db	27	LLVGLVFQISIGIVGVQSVKREKALLSCDYKFCSEEDSHIR--ITYQKDKKKLVSVI--	82	
Qy	71	GKEKFDSVHSKYGRIQSPD-SDSWTLRLNHLNQIKDKGLYOCIIHNKPKPTGIMIRHOMNSE	129	
Db	83	-SGVEPWEWEYKRNIRIVYDIANNYSFSLIGLLDSRGTYTCVQRYGEGSYVVKHLTYVE	140	
Qy	130	LSYLVANSQPELYPIPTNTEYNYIMULTCSSIHGYDEPKKMYL-----LTKNSTIEFYOG	184	
Db	141	LSVRADPPFPNTIESGNPSADIK-RITCPASGGFKRP-RLSWLENGRELNGIMTTF-----	194	
Qy	185	IMQSDNVTLELYDVISLSVSFPDVTSNMTFCLLETDKRLSLSPSSIELEDDPOPPD	244	
Db	195	-----SQDPESELYTISQDLF---MTYDHFIDCFIEYGDAH-VSQNFY--VWVRPEDDPPD	245	
Qy	245	H---IP--W-----ITAVLPVYICVWFYFCILKKKKKKRRPNSTYKCG7	284	
Db	246	EKOIIPFAMAGSAVAKAIIIFIALITIVIAVLAIAIIIIFCIIV-KFRRCRRRN-----	298	
Qy	285	NTMERESQETKK	297	
Db	299	-----EASRETNK	306	

RESULT	15			
ID	062680			
AC	062680;	PRELIMINARY;	PT;	290 AA.
DT	01-NOV-1996 (TREMBLrel. 01,			
DT	01-NOV-1996 (TREMBLrel. 01,			
DT	01-MAY-2000 (TREMBLrel. 13,			
DE	B7-1 (FRAGMENT).			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus			
NP	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MDH; TISSUE=THYMUS;			
RL	Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MDH; TISSUE=THYMUS;			
RL	Judge T.A., Liu M., Tuka L.A.;			
RL	Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: U010925; AAB60503.1; -			
DR	INTERPRO: IPR003006; -			
DR	PRAM: PR00047; 1g; 2.			
DT	CONFLICT			
FT	CONFLICT			

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FT CONFLICT 33 33 F -> L (IN REF. 2).
FT CONFLICT 91 91 E -> K (IN REF. 2).
FT CONFLICT 155 155 S -> Y (IN REF. 2).
FT CONFLICT 213 213 T -> A (IN REF. 2).
FT CONFLICT 237 237 E -> V (IN REF. 2).
FT CONFLICT 250 250 I -> V (IN REF. 2).
FT CONFLICT 257 257 S -> P (IN REF. 2).
FT NON_TER 290 290
SQ SEQUENCE 290 AA: 32691 MW: 479A4B83EF0937C9 CRC64;
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Query Match 12.2%; Score 211; DB 11; Length 290;
Best Local Similarity 26.3%; Pred. No. 2e-10; Indels 48; Gaps 14;
Matches 74; Conservative 51; Mismatches 108;

```
QY 12 ILFVMAFLLSGAAPLKIQAYFNETADLPQCPA-NSQNSLSSELYVFMQDENLVINEVYL 70
DB 27 LLLVGLFQISSGIVGOVSKSVREKALLSCDYKFCSEEOIHR--IYQKHDKMVLSTV-- 82
QY 71 GKKEFDSVHSHKYMGRTSFD-SDSWTLRLHNLQIKDKGLYQCIIHKKPTGMIRIHQMNSE 129
DB 83 --SGVPEVWMEYKKNRYDIANNYSFLGLILSDRGTYTCVQYREGGSYVVKHLTYE 140
QY 130 LSYLANFSOPEIYVFNISNTENVTINLTCSIHGYPEPKKMSVL-----LRTKSTIEYDG 184
DB 141 LSYRADFPPTNITESGNPSADIK-RITCFASGGEPKP-RLSWLENGRELNGINTTI---- 194
QY 185 IMQKSDONTVELYDVGISLSVSFPDVTSMNTIFCILETFDTRILSSPFSIELEDPOPPD 244
DB 195 ----SDDPESELTYTISQLDL-----NTTYDHFICFIEYGDAN-VSQNFTWE-KPPEDPPD 245
QY 245 H---TP--W-----ITAVLPVYIICVWVECL 265
DB 246 EKQTFPFAWAGSDAVKAIIFFTAIPTVIAVIAAIAIIFCI 286
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Search completed: November 6, 2000, 01:45:59
Job time: 2406 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 6, 2000, 00:41:07 ; Search time 649.78 Seconds
(without alignments)
32.132 Million cell updates/sec

Title: US-09-206-132-2
Perfect score: 1733
Sequence: 1 MDPOCTMGISNITLFVMAFL.....AQRVFKSKRTSCDSKSDTCE 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_65: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1733	100.0	329	1 A48754	B7-2 antigen - hum
2	963.5	55.6	330	2 I46691	CD86 precursor - r
3	743.5	42.9	309	2 I49522	gene B7-2 protein
4	243	14.0	309	2 I46690	CD80 precursor
5	243	14.0	309	2 I49503	B-lymphocyte activ
6	222	12.8	321	2 I54766	B-lymphocyte activ
7	201.5	11.6	288	2 A45803	B-cell-restricted
8	187.5	10.8	289	2 G00031	B7 protein - red-c
9	173.5	10.0	487	2 S65133	butyrophilin - mou
10	167	9.6	526	2 S70587	butyrophilin precu
11	162	9.3	526	2 A37821	butyrophilin - bov
12	131.5	7.6	1880	2 T18531	tracilin - medica
13	129.5	7.5	238	2 A46633	Ig lambda-like cha
14	128	7.4	274	2 A47639	OX-2 membrane gly
15	128	7.4	278	1 TDRTOX	OX-2 membrane gly
16	124	7.2	569	2 A46462	T cell activation
17	119.5	6.9	646	2 I38049	cell surface glyco
18	118.5	6.8	391	2 T09058	butyrophilin homol
19	113	6.5	1021	2 I39207	leukocyte surface
20	112.5	6.5	549	2 S04845	Ig heavy chain pre
21	110.5	6.4	994	2 I49276	c-mer tyrosine kin
22	109.5	6.3	230	2 S33161	Ig kappa chain - s
23	108.5	6.3	344	2 I56551	neurotrophin - rat
24	106	6.1	243	2 A53244	leukocyte antigen
25	105	6.0	335	2 S58892	signaling lymphoc
26	104.5	6.0	5175	2 T20992	hypothetical prote
27	104.5	6.0	5198	2 T43290	hemocentin precurs
28	104	6.0	292	2 T44230	hypothetical prote
29	103	5.9	871	1 I48696	protein-tyrosine k

ALIGNMENTS

RESULT 1

A48754

B7-2 antigen - human

N:Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor

C:Species: Homo sapiens (man)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C/Accession: A48754; S39055

R:Freeman, G.J.; Gribben, J.G.; Boussiotis, V.A.; Ng, J.W.; Restifo Jr., V.A.; Lombard

Science 262, 909-911, 1993

A>Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell pr

A/Reference number: A48754; MUID:94053735

A/Accession: A48754

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-329 <FREE>

A/Cross-references: GB:125259; NID:q416368; PIDN:AA58389.1; PID:q416369

A/Note: It is uncertain whether Met-1 or Met-7 is the initiator

R:Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.; Somoza,

Nature 366, 76-79, 1993

A>Title: B70 antigen is a second ligand for CTLA-4 and CD28.

A/Reference number: S39055; MUID:94050123

A/Accession: S39055

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 7-329 <AZU>

A/Cross-references: GB:U04343; NID:q439838; PIDN:AA03814.1; PID:q439839

A/Genetics: GDB:CD86; CD28LG2

A/Cross-references: GDB:433597; OMIM:601020

A/Map position: 3q13.3-3q21

C:Superfamily: B7-2 antigen

C:Keywords: glycoprotein

30	103	5	9	881	1	I48697	protein-tyrosine k
31	102	5	9	931	2	T39143	hypothetical prote
32	101.5	5	9	739	2	S18642	polynucleotide ade
33	101.5	5	9	784	2	T18452	hypothetical prote
34	101	5	8	167	2	T19084	hypothetical prote
35	101	5	8	1274	2	I40813	neurotoxin type F
36	100.5	5	8	416	2	A54017	colon carcinoma-as
37	99	5	7	570	2	A57535	intrileukin 1 recep
38	98.5	5	7	941	1	TVWYMD	protein-tyrosine k
39	98	5	7	588	2	A45254	surface glycoprote
40	98	5	7	664	2	T50316	hypothetical Armad
41	97.5	5	6	285	2	S36903	FC gamma (196) rec
42	97.5	5	6	814	1	A39752	fibroblast-growth
43	97.5	5	6	978	2	S16385	macrophage colony-
44	97	5	6	315	1	HNZVLT	hemagglutinin prec
45	97	5	6	392	1	RWHUPD	poliovirus recepto

Query Match 100.0%; Score 1733; DB 1; Length 329;
Best local similarity 100.0%; Pred. No. 3, 9e-121;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDPOCTMGISNITLFVMAFLGSAAPLKTOAFNFADLPQGFANSONSLSLVVFMODQ	60
DB	1	MDPOCTMGISNITLFVMAFLGSAAPLKTOAFNFADLPQGFANSONSLSLVVFMODQ	60
QY	61	ENLVANEVYLGEKPEFSDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLVQCIIHHKKPTGM	120
DB	61	ENLVANEVYLGEKPEFSDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLVQCIIHHKKPTGM	120
QY	121	IRIHOMNSLSVLANFSOPEIVPISNITENYINLTGSSIHGYEPKMSVLTAKNSTI	180
DB	121	IRIHOMNSLSVLANFSOPEIVPISNITENYINLTGSSIHGYEPKMSVLTAKNSTI	180
QY	181	EVDGIMOKSQDQVTELYNYSISLSVFPDYSNMFTFCILEFDKTRILSSPFSIELEDPQ	240
DB	181	EVDGIMOKSQDQVTELYNYSISLSVFPDYSNMFTFCILEFDKTRILSSPFSIELEDPQ	240

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Db 181 EYDGMOKSDQNTVELYDVSLISVSPDYTSNMTCFICLETDRLLSPFSIELEDPQ 240
QY 241 PPPDHIPWITAVLPYITICVWVFCLILMKKKRRPRNSYKCGTMTMEREESEQTKRK 300
Db 241 PPPDHIPWITAVLPYITICVWVFCLILMKKKRRPRNSYKCGTMTMEREESEQTKRK 300
QY 301 IHIPERSDEAQRVFKSSKTSKSDKSDTCF 329
Db 301 IHIPERSDEAQRVFKSSKTSKSDKSDTCF 329

RESULT 2
I46691
CD86 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 23-Jul-1999
C:Accession: I46691
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecul
A:Reference number: I46689; MUID:95369849
A:Accession: I46691
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-330 <ISO>
A:Cross-references: GB:D49842; NID:g755098; PIDN:BAA08642.1; PID:g755099
C:Superfamily: B7-2 antigen

Query Match 55.6%; Score 963.5; DB 2; Length 330;
Best Local Similarity 58.0%; Pred. No. 3.6e-64;
Matches 192; Conservative 52; Mismatches 84; Indels 3; Gaps 3;

QY 1 MDPOCTMGLSNILFVMAFLSGAAPLKIOAYFNETADLPQCFANSONOSLSELYVFMQDQ 60
Db 1 MDAGCTMGLSVTVYVMAFLLSGAASLRIOAYFNKTDLPQCFNOSRSLSSELYVFMQDQ 60
QY 61 ENLVNELYLGKEKFDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLYOCIIHKKRPTGM 120
Db 61 ERLVLELFGREKPDVNDPKYIGRTSFDQESWNLQLANVQIKDKGYQCFVHHRGAKGL 120
QY 121 IRIHOMSELSVIANFOSPELTPISNTENYINLTCSHIGYEPKRMASVLTAKNSTI 180
Db 121 VPIYOMNSELSVIANFOTPELTLSNTRNSAINLTCSVQGYEPKRMFVLTENATTT 180
QY 181 EYDGMOKSDQNTVELYDVSLISVSPDYTSNMTCFICLETDRLLSPFSIELEDPQ 240
Db 181 EYDGMOKSDQNTVELYDVSLISVSPDYTSNMTCFICLETDRLLSPFSIELEDPQ 240
QY 241 PPPDHIPWITAVLPYITICVWVFCLILMKKKRRPRNSYKCGTMTMEREESEQTKRK 299
Db 241 PVEKPRMLIAAVALTLIVCGIYLFLLMKRKEQOP-GVCECEETIKMDKAENHVEERV 299
QY 300 KIHIPER-SDEAQRVFKSSKTSKSDKSDTCF 329
Db 300 KIHIPERKIPAKAKACEHRLKTPSSDKSAHF 330

RESULT 3
I49522
gene B7-2 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I49522
R:Freeman, G.J.; Bortello, F.; Hodes, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Kim, J.
Exp. Med. 178, 2185-2192, 1993
A:Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell pro
A:Reference number: I49522; MUID:94065585
A:Accession: I49522
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-309 <RES>
A:Cross-references: GB:L25606; NID:g432478; PIDN:AAI9770.1; PID:g432479
```

```
C:Genetics:
A:Gene: B7-2
C:Superfamily: B7-2 antigen

Query Match 42.9%; Score 743.5; DB 2; Length 309;
Best Local Similarity 51.5%; Pred. No. 6.4e-48;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

QY 1 MDPOCTMGLSNILFVMAFLSGAAPLKIOAYFNETADLPQCFANSONOSLSELYVFMQDQ 60
Db 1 MDPOCTMGLSNILFVMAFLSGAAPLKIOAYFNETADLPQCFANSONOSLSELYVFMQDQ 60
QY 61 ENLVNELYLGKEKFDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLYOCIIHKKRPTGM 120
Db 61 OKLVYEHYLGTEKIDSVNAKYLIGRTSPDRNMTLRLHNLQIKDKGYSVDFIQKKRPTGS 120
QY 121 IRIHOMSELSVIANFOSPELTPISNTENYINLTCSHIGYEPKRMASVLTAKNSTI 180
Db 121 ILQOTTELSESVIANFSEPEIKLQNVNGINGINTCTSKQGHKPKRMFLI--TNSTN 178
QY 181 EYDGMOKSDQNTVELYDVSLISVSPDYTSNMTCFICLETDRLLSPFSIELEDPQ 240
Db 179 EYDGMOKSDQNTVELYDVSLISVSPDYTSNMTCFICLETDRLLSPFSIELEDPQ 238
QY 241 PPPDHIPWITAVLPYITICVWVFCLILMKKKRRPRNSYKCGTMTMEREESEQTKRK 298
Db 239 P--QTYWKEITASVVALLVML--LTIYCKKRPNPSRP----SNTASKLERDSNADR 289
QY 299 EKIHPE 305
Db 290 ETINLKE 296
```

```
RESULT 4
I46690
CD80 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999
C:Accession: I46690
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory mole
A:Reference number: I46689; MUID:95369849
A:Accession: I46690
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-299 <ISO>
A:Cross-references: GB:D49843; NID:g755096; PIDN:BAA08643.1; PID:g755097
C:Superfamily: B-1 lymphocyte restricted antigen B7

Query Match 14.0%; Score 243; DB 2; Length 299;
Best Local Similarity 25.8%; Pred. No. 7e-11;
Matches 81; Conservative 65; Mismatches 122; Indels 46; Gaps 14;

QY 3 POCTMGLSNILFVMAFLSGAAPLKIOAYFNETADLPQCFANSONOSLSELYVFMQDQEN 62
Db 12 PCHLHLKLCILALAGHSSGISQYTKYKEMAAALSCDY-NISIDELARMRITYWQKQDQ 70
QY 63 LVINEVYLGKEKFDVSHSKYMGRTSPDSDSWTLRLHNLQIKDKGLYOCIIHKKRPTGM 121
Db 71 MVLS-IISGVE---VWPEYKKNTPFDIINNLSIMILALRLSKGYTYCYVQKNGSFR 126
QY 122 RIHOMNSELSVIANFOSPELTPISNTENYINLTCSHIGYEPK---KMSVLLRTKN 177
Db 127 REHLTSTVLTISIRADFVPVSTIDIGHDPNVK-RIRCSASGSGFEPRLAMWDEEELNAVN 185
QY 178 STIEYDGMOKSDQNTVELYDVSLISVSPDYTSNMTCFICLETDRLLSPFSIELE 237
Db 186 TTYD-----QDLTELKVSSELD---NVTNHNSTYVCLIKGELS-VSIFPMKSP 233
QY 238 DPOPPDHIPWITAVLPYITICVWVFCLILMKKKRRPRNSYKCGTMTMER 289
```

[illegible]

RESULT 6
B-lymphocyte activation antigen 7-1 precursor - rat
154766
C:Species: Rattus norvegicus (Norway rat)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 19-May-2000
C:Accession: U54766
R:JUDGE, T.A.; ILMU, M.; Christensen, P.J.; FAK, J.J.; TURKA, L.A.
Int: Immunol. 7, 171-178, 1995
A>Title: Cloning the rat homolog of the CD28/CTLA-4 ligand B7-1: structural and funct
A:Reference number: 154766; MUID:95252184
A:Accession: 154766
A:Molecule type: mRNA
A:Status: preliminary; translated from GB/EMBL/DBDJ
C:Cross-references: EMBL:U05593; NID:g453381; PIDN:AAA80154.1; PID:g453382
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 12.8%; Score 222, DB 2; Length 321;
Best Local Similarity 25.5%; Pred. No. 2,7e+09;
Matches 83; Conservative 59; Mismatches 116; Indels 68; Gaps 17;

OY 7 MGLSILTVMAFLISGAAPLKIOA-----YNENFADLPICOPA-NSONOSISELVFW 57
 :
Db 14 LGFPRIREFTHLEVLVLLGDISSGIQGVSKSVREKALLSCDYKFCSEDSIHR--ITW 71
OY 58 ODQENMLINEVYLGEKEKFDYSVKYMGRTPSD-SDSWTLRLNLQIKDKGLYOCLIHKK 116
 | :
Db 72 QKHDKMVLSTV----SGPEYWPMPKKNRTVDIANNNVSFLLGLILSDRGHYTCVQRYE 127
OY 117 PTGMIRIHOMNSLSVLANFSOPEIVPISNTENVYINLTSSIHGYPERPKMSVL---- 172
 :
Db 128 GGSYYVKKHITTELVSRDFFPTNPITEYGNSPADIK-RITFEASGGFPKP-RUSMLENGR 165
OY 173 -LRTKNSTIEYDGIMOKSODNATELYDVASISLSVSFPDVTSMNPIFCILETDKRLTSSP 231
 | :
Db 186 ELANGINTTI-----SQDPSELTYTISQLDF---NATYDHFIQDEIERGDAA-VSQN 233
OY 232 FSIEDPDPPDPD---IP-W-----ITANVPVIYICVMYFCILMKWK 271
 | :
Db 234 FT-WVPPEDPDPDEKQTVPFAWAGPDPAVKAILIFPIATVIAYIAAIILIFCITY-KFR 291
OY 272 KKKRPNSKYCGNTMRERESEOTKK 297
 :
Db 292 RCFFRRN-----EASRETNK 306

RESULT 7
A:5803
B-cell-restricted antigen B7 precursor - human
A:Alternate names: B-lymphocyte activation antigen B7
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Sep-1999
C:Accession: U54495; A45803
R:Selyakumar, A.; Moharati, B.K.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B.
Immunogenetics 36, 175-181, 1992
A>Title: Genomic organization and chromosomal location of the human gene encoding the
A:Reference number: U54495; MUID:92307753
A:Accession: U54495
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-288 <RES>
A:Cross-references: GB:M83077; NID:g179327; PIDN:AAA58390.1; PID:g179329
R:Freeman, G.J.; Freedman, A.S.; Segil, J.M.; Lee, G.; Whitman, J.F.; Nadler, L.M.
J. Immunol. 143, 2714-2722, 1989
A>Title: B7, a new member of the Ig superfamily with unique expression on activated a
A:Reference number: A45803; MUID:90010147
A:Molecule type: mRNA

C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 7.5%; Score 129.5; DB 2; Length 238;
Best Local Similarity 23.0%; Pred. No. 0.013;
Matches 53; Conservative 52; Mismatches 99; Indels 33; Gaps 11;
OY 12 ILFWAFLLSG-----AALFKIAQVFNETADLPQFANSONOSISELVFWDQEE--61
DB 7 LIMPLAFVAGIGSDITWQSPVLSVGLQGTATITC-----TASQISYSLAMVYQQRPG 62
OY 62 --NLVNLVYLGKEKFDVSHKYMGRTSFSDSWTLRLHNLQIKDKGLYCIIHHKPPG 119
DB 63 KPSLL--IYATNRKTYGVSERFSG--SGSQTFTLTISVONEDVADYCCSAYGSYSG 117
OY 120 MIRIHNSELVLANFESQPEIVPISNITENVY----INFCSSIHGYPPPKMSVLLRT 175
DB 118 RLAFGR-ETKRLSRSDRQPKLTILPSPDQVQTKGTATLVCLANHFYPELOVQ--WK 173
OY 176 KNSTIEYDGMOKSODNTE-LYDVSISLSVSPDVTSMNTTICILETDKTRLLSPFS 233
DB 174 KDGAIVSDGVQTSNLRASDSTYSVSLTLTSGSDWESNARFSCAL-THVT--LSSPLS 229

RESULT 14

A:7639
OX-2 membrane glycoprotein precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Jun-2000
C:Accession: A47639
R:McCaughan, G.W.; Clark, M.J.; Barclay, A.N.
Immunogenetics 25, 329-335, 1987
A>Title: Characterization of the human homolog of the rat MRC OX-2 membrane glycoprotein
A:Reference number: A47639; MUID:87192943
A:Accession: A47639
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-274 <MCC>
A:Cross-references: GB:X05323; NID:934742; PIDN:CAA28943.1; PID:g1335216; GB:MI7226; GB:
C:Superfamily: MRC OX-2 antigen; immunoglobulin homology
C:Keywords: glycoprotein; membrane protein
F:40-119/Domain: immunoglobulin homology <IMM>

Query Match 7.4%; Score 128; DB 2; Length 274;
Best Local Similarity 21.1%; Pred. No. 0.02;
Matches 63; Conservative 57; Mismatches 120; Indels 58; Gaps 16;
OY 11 NILFWAFLLSGAAPLKI-----QAVFNETADLPQFANSONOSISELVFWDQ--60
DB 13 SLVWMAVAVLCTAQOVVYVODERDYL--TTASLKCSLQNAQ--EALITVWQKKAV 66
OY 61 --ENLVL-----NEVYLGKEKFDVSHKYMGRTSFSDSWTLRLHNLQIKDKGLYCIIHH 114
DB 67 SPENNVTSEHNGVYIGAYKDKINIQGLQNSTITFW-----NITLDEGCYMLFN- 120
OY 115 KKPFGMIRIHNSELVLANFESQPEIVPISNITENVYINLTGSSIHGYPPPKMSVLLR 174
DB 121 --TFEGFKI---SGTACLTIVYQV-IVSLHYKSEDLNITCSAT-ARPA--WVFWK 169
OY 175 TKNSTIEYDGMOKSODNTELYDVSISLSVSPDVTSMNTTIC-ILE--TDKTRLLS 229
DB 170 VPRSGIENSTVTLSPHNTTSVTSI---LHKDPKNQGVKEVICQVYLHGTVDTFQYV 226
OY 230 SPFSIELEDDPPDPDHPWITAVLPYIICVWFCLIMKKKKKKRPRNSYKCGTNTM 287
DB 227 KGWFS-----VPLLSTIVSLVLLVLSILLYM-KRRNDRGELSGOVOKM 273

RESULT 15
TDRKX
OX-2 membrane glycoprotein precursor - rat

N:Alternate names: MRC OX-2 antigen
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 22-Jun-1999
C:Accession: A02114
R:Clark, M.J.; Gagnon, J.; Williams, A.F.; Barclay, A.N.
EMBO J. 4, 113-118, 1985

A>Title: MRC OX-2 antigen; a lymphoid/neuronal membrane glycoprotein with a structure
A:Reference number: A02114; MUID:85257428
A:Accession: A02114
A:Molecule type: mRNA
A:Residues: 1-278 <CLA>
A:Cross-references: GB:X01785; NID:956700; PIDN:CAA25925.1; PID:956701
C:Comment: This protein is found on the surface of neurons, thymocytes, B cells, and
C:Superfamily: MRC OX-2 antigen; immunoglobulin homology
C:Keywords: glycoprotein; surface antigen; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <Sig>
F:31-278/Product: OX-2 membrane glycoprotein #status predicted <MAM>
F:44-123/Domain: immunoglobulin homology <IMM2>
F:153-216/Domain: immunoglobulin homology <IMM2>
F:233-259/Domain: transmembrane #status predicted <TM>
F:260-278/Domain: intracellular #status predicted <INT>
F:51-121,160-214/Disulfide bonds: #status predicted
F:95,103,110,157,181,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.4%; Score 128; DB 1; Length 278;
Best Local Similarity 22.1%; Pred. No. 0.021;
Matches 70; Conservative 53; Mismatches 128; Indels 66; Gaps 16;

OY 3 PQCTWGISNILEFWAFLLSGAAPLKI-----QAVFNETADLPQFANSONOSISELVFW 57
DB 9 PCHLSTYSILMAIAVALSTAGVEVYVODERKILHTTASLRCSLKFTQ--EPLITVW 64
OY 58 QDO-----ENLVL-----LNEVYLGKEKFDVSHKYMGRTSFSDSWTLRLHNLQIKDKGLY 108
DB 65 OKKAVGPEENVVYSKAGVYIOPTYKDRINITELGLNSTITFW-----NTLDEGCY 119
OY 109 QCIHHKPPGMIRIHNSELVLANFESQPEIVPISNITENVYINLTGSSIHGYPPPKR 168
DB 120 MCLF-NMEGSGKV-----SGTACLTIVYQPIVHLHNYFED-HLNTCSAT-ARPA-- 168
OY 169 MSVLLRTKNSITIEYDGMOKSODNTELYDVSISLSVSPDVTSMNTTICIL-----ETD 223
DB 169 -AISWKGSGSIE--NSTESHSHSGT--SVSLIRKDKTKVGVKEVICQVYLIGNVID 224
OY 224 KTRLLSPFSIELEDDPPDPDHPWITAVLPYIICVWFCLIMKKKKKKRPRNSYKCG 283
DB 225 YKQSLDKGFWS-----VPLLSTIVSLVLLVLSILLYM-----KRRN----- 264
OY 284 TMTMRESEBOTKKRK 300
DB 265 ---QERGESSQGMORMK 278

Search completed: November 6, 2000, 01:27:53
Job time: 2806 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 5, 2000, 23:47:27 ; Search time 239.95 Seconds
(without alignments)
22.982 Million cell updates/sec

Title: US-09-206-132-2

Perfect score: 1733
Sequence: 1 MDPOCTMGLSNILFVMAFL.....AQRVFKSKTSCKSDTCF 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 segs, 16761186 residues

Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1733	100.0	329	2	US-08-456-104-2
2	1733	100.0	329	2	US-08-101-624-2
3	1733	100.0	329	3	US-08-479-744A-2
4	1733	100.0	329	4	PCT-US95-02576-23
5	1696	97.9	323	4	PCT-US94-09642-2
6	743.5	42.9	309	3	US-08-456-104-4
7	743.5	42.9	309	3	US-08-479-744A-23
8	743.5	42.9	309	4	PCT-US95-02576-21
9	724.5	41.8	314	4	PCT-US95-02576-13
10	577	33.3	102	3	US-08-479-744A-45
11	517	29.8	100	3	US-08-479-744A-47
12	328	18.9	61	4	PCT-US95-02576-32
13	245.5	14.2	320	4	PCT-US95-02576-17
14	244	14.1	306	4	US-08-147-772-4
15	242	14.0	306	2	US-08-456-104-8
16	242	14.0	306	2	US-08-101-624-25
17	242	14.0	306	3	US-08-153-262-4
18	242	14.0	306	3	US-08-479-744A-31
19	242	14.0	306	3	US-08-147-772-2
20	201.5	11.6	288	2	US-08-456-104-6
21	201.5	11.6	288	2	US-08-101-624-23
22	201.5	11.6	288	2	US-08-751-767A-6
23	201.5	11.6	288	3	US-08-153-262-2
24	201.5	11.6	288	3	US-08-479-744A-29
25	201.5	11.6	288	4	PCT-US95-02576-19
26	185	10.7	208	4	US-08-630-172-15
27	185	10.7	208	4	US-08-724-394A-5
28	160.5	9.3	610	2	US-08-456-104-2

29	159	9.2	342	2	US-08-724-394A-6	Sequence 6, Appl
30	157	9.1	540	2	US-08-724-394A-4	Sequence 4, Appl
31	150	8.7	589	2	US-08-724-394A-1	Sequence 1, Appl
32	132	7.6	212	4	PCT-US95-02576-63	Sequence 63, Appl
33	132	7.6	226	4	PCT-US95-02576-65	Sequence 65, Appl
34	128.5	7.4	200	4	PCT-US95-02576-9	Sequence 9, Appl
35	126.5	7.3	581	4	US-08-724-394A-2	Sequence 2, Appl
36	124	7.2	214	4	PCT-US95-02576-11	Sequence 11, Appl
37	121.5	7.0	581	2	US-08-724-394A-3	Sequence 3, Appl
38	118.5	6.8	365	2	US-08-979-424-3	Sequence 3, Appl
39	107	6.2	242	1	US-08-398-613A-56	Sequence 56, Appl
40	107	6.2	242	1	US-08-398-612A-56	Sequence 56, Appl
41	107	6.2	242	1	US-08-398-611A-56	Sequence 56, Appl
42	107	6.2	242	2	US-08-491-334A-56	Sequence 56, Appl
43	107	6.2	242	3	US-09-027-449-42	Sequence 42, Appl
44	107	6.2	242	3	US-08-804-444A-42	Sequence 42, Appl
45	106.5	6.1	393	1	US-08-429-742-2	Sequence 2, Appl

ALIGNMENTS

```
RESULT 1
US-08-456-104-2
; Sequence 2 APPLIATION US/08456104
; Patent No. 5861310
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nagler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,104
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624;
; FILING DATE: 26-JUL-1993;
; APPLICATION NUMBER: 08/109,393;
; APPLICATION NUMBER: 19-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-456-104-2
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Query Match 100.0%; Score 1733; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.4e-154;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPCQTGSLNILEVNAFLSGAAPLKIOAYENETADLPQOFANSQNSLSELYVFWMDQ 60
DB 1 MDPCQTGSLNILEVNAFLSGAAPLKIOAYENETADLPQOFANSQNSLSELYVFWMDQ 60
QY 61 ENLVNENYVIGKKEKFDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
DB 61 ENLVNENYVIGKKEKFDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
QY 121 IRIHONNSELVLANFSQPEIPIVINSITENYVINTLCCSIHGYPPEPKMSVLLRTKNSTI 180
DB 121 IRIHONNSELVLANFSQPEIPIVINSITENYVINTLCCSIHGYPPEPKMSVLLRTKNSTI 180
QY 181 EYDGIKMSQDNVTELYDVSISSVSFPDVTSMNTIFCLLETDKTRLLSSPFSIELEDPQ 240
DB 181 EYDGIKMSQDNVTELYDVSISSVSFPDVTSMNTIFCLLETDKTRLLSSPFSIELEDPQ 240
QY 241 PPDIHPIWITAVLEPTVILICVMFCLILMKKKRPRNSYKCGTNTMERESQTKRKREK 300
DB 241 PPDIHPIWITAVLEPTVILICVMFCLILMKKKRPRNSYKCGTNTMERESQTKRKREK 300
QY 301 IHIPERSDEAQRVFKSKTSCKDSCTCF 329
DB 301 IHIPERSDEAQRVFKSKTSCKDSCTCF 329

RESULT 2

US-08-101-624-2
Sequence 2, Application US/08101624
Patent No. 5942607
GENERAL INFORMATION
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 5942607el CTLA4/CD28 ligands and
TITLE OF INVENTION: Uses therefor
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/101,624
FILING DATE: 26-JUL-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-101-624-2

Query Match 100.0%; Score 1733; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 2,4e-154;

Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDPCQTGSLNILEVNAFLSGAAPLKIOAYENETADLPQOFANSQNSLSELYVFWMDQ 60
DB 1 MDPCQTGSLNILEVNAFLSGAAPLKIOAYENETADLPQOFANSQNSLSELYVFWMDQ 60
QY 61 ENLVNENYVIGKKEKFDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
DB 61 ENLVNENYVIGKKEKFDVSHSKYMGRTSPDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
QY 121 IRIHONNSELVLANFSQPEIPIVINSITENYVINTLCCSIHGYPPEPKMSVLLRTKNSTI 180
DB 121 IRIHONNSELVLANFSQPEIPIVINSITENYVINTLCCSIHGYPPEPKMSVLLRTKNSTI 180
QY 181 EYDGIKMSQDNVTELYDVSISSVSFPDVTSMNTIFCLLETDKTRLLSSPFSIELEDPQ 240
DB 181 EYDGIKMSQDNVTELYDVSISSVSFPDVTSMNTIFCLLETDKTRLLSSPFSIELEDPQ 240
QY 241 PPDIHPIWITAVLEPTVILICVMFCLILMKKKRPRNSYKCGTNTMERESQTKRKREK 300
DB 241 PPDIHPIWITAVLEPTVILICVMFCLILMKKKRPRNSYKCGTNTMERESQTKRKREK 300
QY 301 IHIPERSDEAQRVFKSKTSCKDSCTCF 329
DB 301 IHIPERSDEAQRVFKSKTSCKDSCTCF 329

RESULT 3

US-08-479-744A-2
Sequence 2, Application US/08479744A
Patent No. 6084067
GENERAL INFORMATION
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6084067el CTLA4/CD28 ligands and
TITLE OF INVENTION: Uses therefor
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,744A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
APPLICATION NUMBER: 08/109,393
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-744A-2

Query Match 100.0%; Score 1733; DB 3; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.4e-154;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPOCTMGLSNILFVMAFLILSGAAPLKIQAYFNETADLPQCFANSQNSLSLVLVFWMDQ 60
DB 1 MDPOCTMGLSNILFVMAFLILSGAAPLKIQAYFNETADLPQCFANSQNSLSLVLVFWMDQ 60
QY 61 ENLVNVEVYLGKREKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
DB 61 ENLVNVEVYLGKREKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
QY 121 IRIHOMNSELVLANFQPEIIVPISNITENYINLTCSIHGYPEPKKMSVLLRTKNSTI 180
DB 121 IRIHOMNSELVLANFQPEIIVPISNITENYINLTCSIHGYPEPKKMSVLLRTKNSTI 180
QY 181 EYDGIKMSQDNVTELYDVSTISLSVSPDYTSNMRTIFCILETDKTRLLSPFSIELEDPQ 240
DB 181 EYDGIKMSQDNVTELYDVSTISLSVSPDYTSNMRTIFCILETDKTRLLSPFSIELEDPQ 240
QY 241 PPPDHIMTITAVLPTVIICVWFCLILMKKKRRPRNSYKCGTNTMERESDQTKRKREK 300
DB 241 PPPDHIMTITAVLPTVIICVWFCLILMKKKRRPRNSYKCGTNTMERESDQTKRKREK 300
QY 301 IHIPERSDEAORVFKSSKTSKCDKSDTCF 329
DB 301 IHIPERSDEAORVFKSSKTSKCDKSDTCF 329

RESULT 4
PCT-US95-02576-23
Sequence 23, Application PC/TUS9502576
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02576
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120CPCPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
PCT-US95-02576-23

Query Match 100.0%; Score 1733; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.4e-154;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPOCTMGLSNILFVMAFLILSGAAPLKIQAYFNETADLPQCFANSQNSLSLVLVFWMDQ 60
DB 1 MDPOCTMGLSNILFVMAFLILSGAAPLKIQAYFNETADLPQCFANSQNSLSLVLVFWMDQ 60
QY 61 ENLVNVEVYLGKREKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
DB 61 ENLVNVEVYLGKREKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGM 120
QY 121 IRIHOMNSELVLANFQPEIIVPISNITENYINLTCSIHGYPEPKKMSVLLRTKNSTI 180
DB 121 IRIHOMNSELVLANFQPEIIVPISNITENYINLTCSIHGYPEPKKMSVLLRTKNSTI 180
QY 181 EYDGIKMSQDNVTELYDVSTISLSVSPDYTSNMRTIFCILETDKTRLLSPFSIELEDPQ 240
DB 181 EYDGIKMSQDNVTELYDVSTISLSVSPDYTSNMRTIFCILETDKTRLLSPFSIELEDPQ 240
QY 241 PPPDHIMTITAVLPTVIICVWFCLILMKKKRRPRNSYKCGTNTMERESDQTKRKREK 300
DB 241 PPPDHIMTITAVLPTVIICVWFCLILMKKKRRPRNSYKCGTNTMERESDQTKRKREK 300
QY 301 IHIPERSDEAORVFKSSKTSKCDKSDTCF 329
DB 301 IHIPERSDEAORVFKSSKTSKCDKSDTCF 329

RESULT 5
PCT-US94-09642-2
Sequence 2, Application PC/TUS9409642
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: Purified Mammalian CTLA-4 Binding
TITLE OF INVENTION: protein and Related Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation, M-3-W
STREET: One Giralda Farms
CITY: Madison
STATE: New Jersey
COUNTRY: USA
ZIP: 07940-1000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh IIfx
OPERATING SYSTEM: System Software 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09642
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/120,606
FILING DATE: 13-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,882
FILING DATE: 03-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Blasdale, John H. C.
REGISTRATION NUMBER: 31,895
REFERENCE/DOCKET NUMBER: DX0390K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-822-7398
TELEFAX: 201-822-7039
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-09642-2

Query Match 97.9%; Score 1696; DB 4; Length 323;
Best Local Similarity 100.0%; Pred. No. 6.8e-151;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MGSLNITLFFVNAFLLSGAAPLKIAQYFNETADLPQCFANSONOSLSLAVFMQDQEMVLN 66
DB 1 MGSLNITLFFVNAFLLSGAAPLKIAQYFNETADLPQCFANSONOSLSLAVFMQDQEMVLN 60
QY 67 EYVIGKREKFDVSHSKYMGRTSPDSQSWTLRLHNLQIKDKGLYOCIIHHKKPTGMIRIHOM 126
DB 61 EYVIGKREKFDVSHSKYMGRTSPDSQSWTLRLHNLQIKDKGLYOCIIHHKKPTGMIRIHOM 120
QY 127 NSELVLANFSQPEIPIVINSITENVYINLCCSIHGYPEPKKMSVLLRTKNSITIEDGIM 186
DB 121 NSELVLANFSQPEIPIVINSITENVYINLCCSIHGYPEPKKMSVLLRTKNSITIEDGIM 180
QY 187 QKSDQNTVELYDVSISSVSEFPDVTSMNITFCILETDKTRLLSSPSIELEDPQPPDHI 246
DB 181 QKSDQNTVELYDVSISSVSEFPDVTSMNITFCILETDKTRLLSSPSIELEDPQPPDHI 240
QY 247 PMTAVLPPTYIICVWVFLILMKKKRRNSYKCGTNTMERESSEOTKKREKHIPER 306
DB 241 PMTAVLPPTYIICVWVFLILMKKKRRNSYKCGTNTMERESSEOTKKREKHIPER 300
QY 307 SDEARVFKSKTSKCDKSDTCE 329
DB 301 SDEARVFKSKTSKCDKSDTCE 323

RESULT 6
US-08-456-104-4
Sequence/4, Application US/08456104
Patent No. 5861310

GENERAL INFORMATION:

APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
City: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,104
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109,393;
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-456-104-4

Query Match 42.9%; Score 743.5; DB 2; Length 309;
Best Local Similarity 51.5%; Pred. No. 8.1e-62;
Matches 158; Conservative 45; Mismatches 91; Indels 13; Gaps 5;

QY 1 MDPCCTMGSLNITLFFVNAFLLSGAAPLKIAQYFNETADLPQCFANSONOSLSLAVFMQDQ 60
DB 1 MDPCCTMGSLNITLFFVNAFLLSGAAPLKIAQYFNETADLPQCFANSONOSLSLAVFMQDQ 60
QY 61 ENLYANVYIGKREKFDVSHSKYMGRTSPDSQSWTLRLHNLQIKDKGLYOCIIHHKKPTGM 120
DB 61 QKLVYEHYIGTEKLDVSHSKYMGRTSPDSQSWTLRLHNLQIKDKGLYOCIIHHKKPTGM 120
QY 121 IRIHOMNSELVLANFSQPEIPIVINSITENVYINLCCSIHGYPEPKKMSVLLRTKNSIT 180
DB 121 IRIHOMNSELVLANFSQPEIPIVINSITENVYINLCCSIHGYPEPKKMSVLLRTKNSIT 180
QY 181 EYDGINQKSDQNTVELYDVSISSVSEFPDVTSMNITFCILETDKTRLLSSPSIELEDPQ 240
DB 179 EYDGINQKSDQNTVELYDVSISSVSEFPDVTSMNITFCILETDKTRLLSSPSIELEDPQ 238
QY 241 PPPDHIPW--ITAVLPPTYIICVWVFLILMKKKRRNSYKCGTNTMERESSEOTKKR 298
DB 239 PPPDHIPW--ITAVLPPTYIICVWVFLILMKKKRRNSYKCGTNTMERESSEOTKKR 289
QY 299 EKHITPE 305
DB 290 EKHITPE 296

RESULT 7
US-08-479-744A-23
Sequence 23, Application US/08479744A
Patent No. 6084067

GENERAL INFORMATION:

APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6084067e1 CTLA4/CD28 Ligands and
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
City: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,744A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
APPLICATION NUMBER: 08/109,393
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/147,773


```

? REFERENCE/DOCKET NUMBER: BMT-120CPBC
?
? TELECOMMUNICATION INFORMATION:
?
? TELEPHONE: (617)227-7400
?
? TELEFAX: (617)227-5941
?
? INFORMATION FOR SEQ. ID NO: 13:
?
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 314 amino acids
?
? TYPE: amino acid
?
? TOPOLOGY: linear
?
? MOLECULE TYPE: protein
?
PCT-US95-02576-13

```



```
REFERENCE/DOCKET NUMBER: RPI-004CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-744A-47

Query Match
Best Local Similarity 100.0%; Score 517; DB 3; Length 102;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 ANFSQPEIVPISNITENYINLTGSSIHGYPPPKMSVLTAKNSTIEYDGIQKSDNY 193
1 ANFSQPEIVPISNITENYINLTGSSIHGYPPPKMSVLTAKNSTIEYDGIQKSDNY 60
DB 1 ANFSQPEIVPISNITENYINLTGSSIHGYPPPKMSVLTAKNSTIEYDGIQKSDNY 60
QY 194 TELYDVISISVSFPDVTSMNTIFCLTETDKTRLSSPFSIE 235
61 TELYDVISISVSFPDVTSMNTIFCLTETDKTRLSSPFSIE 102
DB 61 TELYDVISISVSFPDVTSMNTIFCLTETDKTRLSSPFSIE 102

RESULT 12
PCT-US95-02576-32
Sequence 32, Application PC/TUS9502576
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02576
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandiagouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BMT-120CPPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-02576-32

Query Match
Best Local Similarity 100.0%; Score 328; DB 4; Length 61;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 KWKKKRPNRSYKCGTNTMERESQTKRKRIHIPERSDEARVFKSSKTSCKSDKSDTC 328
```

```
|||||
DB 1 KWKKKRPNRSYKCGTNTMERESQTKRKRIHIPERSDEARVFKSSKTSCKSDKSDTC 60
QY 329 F 329
DB 61 F 61

RESULT 13
PCT-US95-02576-2
Sequence 2, Application PC/TUS9502576
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02576
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandiagouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BMT-120CPPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-02576-2

Query Match
Best Local Similarity 14.2%; Score 245.5; DB 4; Length 320;
Matches 82; Conservative 51; Mismatches 100; Indels 37; Gaps 14;

QY 11 NILEVNAFLISGAAPLKIAFYNETAD--LPCQFANSQNSLSLTVFWQOENLYVNE 67
22 NILEVNLIRLSQVSDVDQLSKSVKDKVLPORY-NSPHEDESERIRYWKQHDVVLVS- 79
DB 22 NILEVNLIRLSQVSDVDQLSKSVKDKVLPORY-NSPHEDESERIRYWKQHDVVLVS- 79
QY 68 VYLGKREKFDVSHKVMGRSPDSWTLHLNLOIQDKGLYOCIIHHKKPTGMIRI-HQM 126
80 VYLGKRLK--VWPEYKRNRLYDNTYSLIILGLVLSDRGTYSVV-OKKERGTVEYKHIA 135
DB 80 VYLGKRLK--VWPEYKRNRLYDNTYSLIILGLVLSDRGTYSVV-OKKERGTVEYKHIA 135
QY 127 NSELSVLANFSQPEIVPISNITENYINLTGSSIHGYPPPKMSVLTAKNSTIEYDGIQKSDNY 181
136 LVKLSIKADSTNTNITESGSPADTK-RITCFASGGFPKP-RFSLWENGRELPGIWTI- 192
DB 136 LVKLSIKADSTNTNITESGSPADTK-RITCFASGGFPKP-RFSLWENGRELPGIWTI- 192
QY 182 YDGIQKSDNYTELVDVSISSVSFPDVTSMNTIFCLTETDKTRLSSPFSIELEDPQP 241
193 -----SQPSELEYTISSQIDF---NTRNTIKCLIKYGDAR-VSDFIWE-KRPED 240
DB 193 -----SQPSELEYTISSQIDF---NTRNTIKCLIKYGDAR-VSDFIWE-KRPED 240
QY 242 PPDHLPWIT-----AVLPYIICVWVFC 264
241 PPDHLPWIT-----AVLPYIICVWVFC 270
DB 241 PPDHLPWIT-----AVLPYIICVWVFC 270
```

RESULT 14

PCT-US95-02576-17
Sequence 17, Application PC/TUS9502576
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02576
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BMT-1200PPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-02576-17

Query Match 14.1%; Score 244; DB 4; Length 306;
Best Local Similarity 27.9%; Pred. No. 4.2e-15;
Matches 89; Conservative 58; Mismatches 120; Indels 52; Gaps 16;

12 ILFVAFILSGAFLKIAVYNETAD---LPCOPANSONOSLSLVYFMDQENLVANEY 68
13 LLEVLILRLSYSSDVDDQLSKSVKDKVLLPCRY-NSPHDESEDRILYWKHDKVYLS-V 80
69 YLGEKEFDSVSHKYMGARTSPDSWMTLRLNLTQIKDKGLYOCILIHKKPGMIRI-HQNM 127
81 IAGKLK---VMEYKRNRLYDNTTYSLITGLVLSDRGTVSCVY-QKKRGTYEVKHLAL 136
128 SELSLANFSQPELYPINTEENYINLTCSSINGYPERPKMSYL-----LRRKNTIEE 182
137 VKLSIKAFSPNITSGSPADKR-RTGCFASGFPKP-RFSWLENGRELPGINNTI-- 192
183 DGIKMSODNTLEYDVASISLSVSPDVTSMNTIFCILETDTKTLSSPSIELEDPQPP 242
193 -----SDPSELEYTISQDLE---NTRNHTIKCLIKYGDAN-VSEDTWE-KPPEDP 241
243 PDHITWIT-----AVLPYILCVWFCLILMKWKKKKRRNSYKCGTMTMERESQOT 295
244 PDSKNTLVLFAGAGCAVTIVYVVIKQFC-----KRRSCFR-----RNSASRE 286
296 KKREKIHIPERSDEAQRVF 314
287 TNNSLTFGPEALAEQIVF 305

RESULT 15

US-08-147-772-4
Sequence 4, Application US/08147772
Patent No. 5858776
GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasubramanian
APPLICANT: Glimcher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells with Increased Immunogenicity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,772
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B lymphocyte activation antigen; Ig
DESCRIPTION: via activation of CD28 pathways, binds to CD28+
DESCRIPTION: T cells, transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -37 to -1
IDENTIFICATION METHOD: similarity with known
OTHER INFORMATION: sequence
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 210
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 211 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular (cytoplasmic) domain
LOCATION: 236 to 269
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 105
IDENTIFICATION METHOD: similarity with known

XX	
PN	W09503408-A.
XX	
PD	02-FEB-1995.
XX	
PE	26-JUL-1994; 94MO-US08423.
XX	
PR	26-JUL-1993; 93US-0101624.
PR	19-AUG-1993; 93US-0109393.
XX	
PR	03-NOV-1993; 93US-0147773.
XX	
PA	(DAND) DANA FARBER CANCER INST INC.
PA	(REPK) REPLIGEN CORP.
XX	
PI	Freeman GJ, Gray GS, Greenfield E, Nadler LM;
XX	
DR	WPI: 1995-075236/10.
XX	
DR	N-FSDB: Q81351.
XX	
PT	Nucleic acids encoding CTLA4/CD28 counter receptor. 87-2 - useful
PT	for enhancing or suppressing T-cell mediated immune responses
XX	
PS	Claim 35; Fig 8; 175pp; English.

CC A cDNA library was constructed using the pCDM8 vector using poly A+ RNA
CC from the human anti-19M activated B cells. Four clones were strongly
CC positive for Br-2 expression by indirect immunofluorescence using
CC CTRM41g and flow cytometric analysis. The Br-2 cDNA insert in clone
CC 29 was sequenced in the pCDM8 expression vector employing the
CC following strategy. Initial sequencing was performed using
CC sequencing primers 17 (081352), CDM8R (081353) (Invitrogen) homologous
CC to pCDM8 vector sequences adjacent to the clone Br-2 cDNA. Sequencing
CC was performed using dye terminator chemistry and an ABI automated DNA
CC sequencer. DNA sequence obtained, using these primers was used to design
CC additional sequencing primers (see 081354-081363). This cycle of
CC sequencing and selection of additional primers was continued until
CC the Br-2 cDNA was completely sequenced on both strands. The human
CC Br-2 clone 29 cDNA sequence is given in 081351. The predicted
CC protein sequence (R67984) exhibits many features common to other
CC type 1 Ig superfamily membrane proteins. Following cleavage of the
CC signal peptide the resulting membrane-bound protein would have an
CC unmodified mol. wt. of approx. 34 kDa. The extracellular domain
CC contains eight potential N-linked glycosylation sites. E. coli
CC transformed with a vector contg. the cDNA insert of clone 29 was
CC deposited under ATCC 69357 on July 26 1993.

Query Match	100.0%	Score 1733;	DB 16;	Length 329;
Best Local Similarity	100.0%	Pred. No. 4.2e-151;		
Matches 329; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MDPCTMGISNLNLFMAVFLISGAAPLKIQAFFENFADIPCOFANSQNSISLSELYWMDQ	60	
Db	1	mnpqctmgisnlifmalisgaaplkiqayfneadipcqfansqnsiselvftwdq	60	
QY	61	ENLVLENYLYGKEKFDVSHSKYMGRTSPDSQSWTLRLNLQIKDGLQCIIRHKKPPGM	120	
Db	61	enlvlnenylygkefcdvshskymgrtstdsawtlrlmlqdkdqlgycilnhkppgpm	120	
QY	121	IRIHQMSLSVLANSOPETVPIPSNITENYINLTCSHIGYEPKPKMSVLLRTKNSIT	180	
Db	121	irihqmselsvlansfqspeivpislntenyinltcsahgypkpkmsvllrtknsit	180	
QY	181	EYDSIMQSQNWEHLDVYSISLSPFDVTSNMTIFCILETDKTRILSSPSTIELEDPQ	240	
Db	181	eydimgksgqndvelydvasislsvsfpdvsnmtifciletdktrilsspsfielepq	240	
QY	241	PPPHIMFMTAVLEVTYIICVAVFCLILMKMKKKKRRPRRSTYCGNTWPRESEQTKRKEK	300	
Db	241	ppphimfwtavleptviicvnmvfcililwkwkkrkrrprmsycqntnereseqtkkrkek	300	

XX MO9640915-A2.
PN 19-DEC-1996.
PD 06-JUN-1996; 96WO-US09052.
XX 07-JUN-1995; 95US-0479744.
XX (DAND) DANA FARBER CANCER INST INC.
PA (REPK) REPLIGEN CORP.
XX Freeman GJ, Gray GS, Nadler LM;
PI WPI: 1997-077269/07.
XX N-PSDB: 749181.
DR DNA encoding a B7-2 fusion protein - used to enhance or down
PT regulate B lymphocyte antigens
XX
XX Claim 4; Page 95-96; 171pp; English.
PS
XX Human B-lymphocyte antigen B7-2 (W08467) is a CTLA4/CD28 ligand
CC which costimulates T cell activation. It shows 26% amino acid
CC identity to human B7-1. Its sequence was deduced from a cDNA
CC clone (T49181) isolated from an anti-IGM activated B cell cDNA
CC library. Novel fusion proteins comprising the extracellular domain,
CC variable region-like or constant region-like domains of B7-2 (see
CC also W08472-73) and e.g. an immunoglobulin heavy chain constant
CC region can be expressed in host cells and used to enhance or
CC suppress T cell-mediated immune responses.
CC
XX
SQ Sequence 329 AA;

Query Match 100.0%; Score 1733; DB 18; Length 329;
Best Local Similarity 100.0%; Pred. No. 4.2e-151;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDPQCTMGLSNIIFVMAFLSLGAPLKIQAIFNETADLPQCFANSONOSLSELVFMQDQ 60
DB 1 mdpqctmglsnllfvmatlsgaaplikqayfnetadlpqcfansqngsiseivfwqdg 60
OY 61 ENLVANEVYLGEKEKFDSDVSHSKYMGRTSPDSWTLRLNLQIKDKGLYOCIIHKKRPTGM 120
DB 61 enlvanevylgkfkdsdvshskymgrtsfdsdswtlrlnlqikdkglyociihkkpctgm 120
OY 121 IRIHQMSSELAVANFSQPEIPIISNTITENVYINLTCSHIGYPERKMSVLLRTKNSTI 180
DB 121 irihqmselsvlnfsopeiipisntitenyintltcsshigyperkmsvllrtknsti 180
OY 181 EYDGMQSDQNTVELYVSISSVSPDVTSNMNITFCILETQKTRLLSPFSIELEDPO 240
DB 181 eydgmqsqdnvteilydvsissvsfpdvtsnmnifciletdktrllspfsieleddp 240
OY 241 PPPDHIPMTAVLPTVITICVWVECLIMKWKKKRPNRSYKCGTNTMERESQTKKREK 300
DB 241 pppdhipmtavlpvtviticvwvfcilimkwkkkrrpnrsykcgtnumereesqtkkrek 300
OY 301 IHIPEBSDEAQRVFKSKTSCKSDKSDTCF 329
DB 301 ihlperdeagrvfkssktscksdctcf 329

RESULT 3
ID W73638 standard; Protein; 329 AA.
XX
AC W73638;
XX
DT 23-MAR-1999 (first entry)
XX
DE Human B7-2 antigen.

XX B7-2 antigen; mammalian tumour cell; T cell costimulation; CD28 ligand;
KM CTLA4 ligand; therapy; T-cell response; human.
XX Homo sapiens.
XX OS
XX US5861310-A.
XX
XX 19-JAN-1999.
XX
XX 30-MAY-1995; 95US-0456104.
XX
XX 30-MAY-1995; 95US-0456104.
XX
XX 03-NOV-1993; 93US-0147773.
XX
XX (DAND) DANA FARBER CANCER INST INC.
XX
XX Freeman GJ, Gray GS, Nadler LM;
XX
XX WPI: 1999-130394/11.
XX
XX N-PSDB: V55784.
XX
XX Tumour cell transfected to express B7-2 molecule - useful for tumour
PT therapy by stimulating T-cell response
XX
XX Claim 10; Column 27-30; 27pp; English.
PS
XX This sequence is the human B7-2 antigen, which can be used in the
CC method of the invention. The method is for transfecting an isolated
CC mammalian tumour cell with an exogenous nucleic acid molecule encoding a
CC mammalian B7-2 molecule, where the B7-2 molecule is expressed in the
CC tumour cell is capable of costimulating a T cell and is capable of
CC binding a CD28 or CTLA4 ligand. The method is useful for treating tumours
CC by stimulating a T-cell response against tumour cells in vivo.
CC
XX
SQ Sequence 329 AA;

Query Match 100.0%; Score 1733; DB 20; Length 329;
Best Local Similarity 100.0%; Pred. No. 4.2e-151;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDPQCTMGLSNIIFVMAFLSLGAPLKIQAIFNETADLPQCFANSONOSLSELVFMQDQ 60
DB 1 mdpqctmglsnllfvmatlsgaaplikqayfnetadlpqcfansqngsiseivfwqdg 60
OY 61 ENLVANEVYLGEKEKFDSDVSHSKYMGRTSPDSWTLRLNLQIKDKGLYOCIIHKKRPTGM 120
DB 61 enlvanevylgkfkdsdvshskymgrtsfdsdswtlrlnlqikdkglyociihkkpctgm 120
OY 121 IRIHQMSSELAVANFSQPEIPIISNTITENVYINLTCSHIGYPERKMSVLLRTKNSTI 180
DB 121 irihqmselsvlnfsopeiipisntitenyintltcsshigyperkmsvllrtknsti 180
OY 181 EYDGMQSDQNTVELYVSISSVSPDVTSNMNITFCILETQKTRLLSPFSIELEDPO 240
DB 181 eydgmqsqdnvteilydvsissvsfpdvtsnmnifciletdktrllspfsieleddp 240
OY 241 PPPDHIPMTAVLPTVITICVWVECLIMKWKKKRPNRSYKCGTNTMERESQTKKREK 300
DB 241 pppdhipmtavlpvtviticvwvfcilimkwkkkrrpnrsykcgtnumereesqtkkrek 300
OY 301 IHIPEBSDEAQRVFKSKTSCKSDKSDTCF 329
DB 301 ihlperdeagrvfkssktscksdctcf 329

RESULT 4
ID R71478 standard; Protein; 323 AA.
XX
AC R71478;
XX

```
DT 09-OCT-1995 (first entry)
XX
DE B70 type B antigen which binds CTLA-4 and CD28.
XX
KM B70 antigen; CTLA-4; CD28; T cell response.
XX
OS Homo sapiens.
XX
PN W09506738-A.
XX
PD 09-MAR-1995.
XX
PF 02-SEP-1994; 94MO-US09642.
XX
PR 03-SEP-1993; 93US-0116882.
XX
PR 13-SEP-1993; 93US-0120606.
XX
PA (AZUM/) AZUMA M.
PA (OKUM/) OKUMURA K.
PA (SCHE ) SCHERING CORP.
XX
PI Azuma M, Lanier LL, Okumura K, Phillips JH;
PI Somoza Diaz-Sarmiento M;
XX
DR WPI: 1995-115453/15.
DR N-PSDB; Q85873.
XX
XX
XX New CTLA-4/CD28 binding protein, B70 - used to develop prods for
PT modulating the physiology, growth or development of cells.
XX
XX
XX Claim 3; Page 44-45; 55pp; English.
XX
XX B70 is a natural proteinaceous binding partner for CTLA-4 and CD28
CC markers/antigens. It is distinct from the known B7/BBI marker. It is
CC representative of 'type B' markers/antigens/binding partners. The
CC type A markers/binding partners include both CTLA-4 and CD28 and
CC antibodies specific for B70, and are characterised, in part, by the
CC property of serving as a binding partner for B70. A cDNA encoding a
CC B70 antigen was cloned by expression cloning using mAb IT2.236 to
CC select COS7 cells transfected with a cDNA library cloned into the
CC pEF4 vector. The library was made from RNA isolated from a human
CC EBV-transformed B-lymphoblastoid cell line JY.
XX
XX
SQ Sequence 323 AA;
XX
XX
XX Query Match 97.9%; Score 1696; DB 16; Length 323;
XX Best Local Similarity 100.0%; Pred. No. 1e-147;
XX Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 7 MGSLNILEVNAFLISGAAPLKIQAYFNETADLPQOFANSONOSISELVVFMQDOENLVN 66
XX 1 mgsnllfmaflisgaaplkiaqayfnetadlpqofansqngslselvfwqdenlvn 60
XX
XX 67 EYVLGKEKFDVSHSKYWGRTSFDSDSWTLRLHNLQIKDKGLYOCIIHKKPTGMIRIHQM 126
XX 61 evylgkekfdsvshskymgrtsfdsdswtlrlhnlqikdkglyocilhhkptgmirihgm 120
XX
XX 127 NSLSVLANSPQPEIVPISNITENVYINLTCSSIHGVPPEKKMSVLLRTNSTIETDGIIM 186
XX 121 nselsvlanspqpeivpislntenylnltcssihgyppkkmsvllrtknstleyqim 180
XX
XX 187 OKSODNWTLEYDVYSISVSFPPVTSNMTFICILETPDKTLLSSPSEILEDQPPDH 246
XX 181 qksqdnwtleydvysisvsfpvtsnmtficletpdktrllsspsieleqppppdh 240
XX
XX 247 PWTAVLPVVIICVMVFCILIMWKKKKRPKNRSYKCGTNTMERESQTKRKREKIHIPER 306
XX 241 pwtavlpvviicvmvfcilimwkkkkrrpnsykcgtntmeresqtkrkrekibper 300
XX
XX 307 SDEAQRFVFKSSKSSGDKSDTCF 329
XX 301 sdeaqrfvfkssksscdkscdtcf 323
XX
XX
```

```
RESULT 5
ID Y44290
XX Y44290 standard; Protein; 323 AA.
XX
XX Y44290;
XX
XX 29-FEB-2000 (first entry)
XX
XX Human B7.2 co-stimulatory molecule.
XX
XX Human B7.2 co-stimulatory molecule; antigen presenting cell;
XX immune response; cell surface receptor; Major histocompatibility complex;
XX MHC classII; proton motor force; mitochondrial membrane potential;
XX mitochondrial metabolism; cancer; autoimmune disease; glycoprotein;
XX neurodegenerative disorder.
XX
XX OS Homo sapiens.
XX
XX PN W09953953-A2.
XX
XX PD 28-OCT-1999.
XX
XX PF 30-MAR-1999; 99MO-US06874.
XX
XX PR 17-APR-1998; 98US-0082250.
XX PR 29-JUL-1998; 98US-0094519.
XX PR 24-SEP-1998; 98US-0101580.
XX
XX PA (UYVE-) UNIV VERMONT.
XX
XX PI Newell MK;
XX
XX DR WPI: 2000-096773/08.
XX DR N-PSDB; Z29321.
XX
XX
XX Use of cell surface and membrane characteristics for developing
PT products for treating cancers, autoimmune diseases or neurodegenerative
PT diseases -
XX
XX PS Disclosure; Page 116-117; 123pp; English.
XX
XX
XX The present sequence is human B7.2 co-stimulatory molecule. This is
CC a glycoprotein on the surface of antigen presenting cells. This is
CC involved in stimulation of an immune response by its ability to interact
CC with various immune cell surface receptors. The regulation of cell
CC surface expression of MHC classII and co-stimulatory molecule B7 can be
CC manipulated by regulating the intracellular dissipation of proton motor
CC force which can be assessed in terms of mitochondrial membrane potential.
CC These methods can be used for regulating cell growth and division to
CC control disease processes by manipulating mitochondrial metabolism and
CC the expression of cell surface immune proteins. They can be used for
CC treating diseases associated with excessive cellular division, aberrant
CC differentiation, and premature cellular death, e.g. cancers, autoimmune
CC diseases, neurodegenerative disorders etc.
XX
XX
SQ Sequence 323 AA;
XX
XX
XX Query Match 97.9%; Score 1696; DB 21; Length 323;
XX Best Local Similarity 100.0%; Pred. No. 1e-147;
XX Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 7 MGSLNILEVNAFLISGAAPLKIQAYFNETADLPQOFANSONOSISELVVFMQDOENLVN 66
XX 1 mgsnllfmaflisgaaplkiaqayfnetadlpqofansqngslselvfwqdenlvn 60
XX
XX 67 EYVLGKEKFDVSHSKYWGRTSFDSDSWTLRLHNLQIKDKGLYOCIIHKKPTGMIRIHQM 126
XX 61 evylgkekfdsvshskymgrtsfdsdswtlrlhnlqikdkglyocilhhkptgmirihgm 120
XX
XX 127 NSLSVLANSPQPEIVPISNITENVYINLTCSSIHGVPPEKKMSVLLRTNSTIETDGIIM 186
XX
```



```

Db 121 nselsvlafspgelvpslntlenylnltcsslbgyppepkmsvllrknstleydgm 180
QY 167 QKSQNMVELYVSVISLSVSPDYVSNMTIFCLLETDKTRLISPPSTLEDPDPPDH 246
Db 161 qksqdvteilydvsislsvsfpvtsmnltfclletdktrllsspfslsleddppppdh 240
QY 247 PWITAVLPVLIICVAVFCLILMKMKKKRPRNSYKGTNTMRESEQTKRKREKTHIPER 306
Db 241 pwitavlpvliicvavfclilmkmkkkripnsykcgtntmeresegtkrkrehlhp 300
QY 307 SDEAQRVFRSSKRTSSCDKSDTCF 329
Db 301 sdeaqrvfrsskrtsscdskdctcf 323

RESULT 6
W42339
ID W42339 standard; Protein; 260 AA.
XX
AC W42339;
XX
DT 22-JUN-1998 (first entry)
DE CD86 extracellular domain.
XX
KW Hexameric fusion protein; IgA; alpha-tp; tailpiece; antibody;
KW CD86; CTLA-4; vaccine; diagnosis; binding assay; screening;
KW human; ds.
XX
OS Homo sapiens.
XX
FH Key
FT Peptide
FT Protein
FT Peptide
FT Peptide
XX
PN W09747732-A2.
XX
PD 18-DEC-1997.
XX
PE 13-JUN-1997; 97WO-US12599.
XX
PR 21-FEB-1997; 97US-0038915.
PR 14-JUN-1996; 96US-0019934.
PR 19-FEB-1997; 97US-0043948.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Chaikin MA, Lyn SDP, Sweet RW, Truneh A;
XX
DR WPI; 1998-052299/05.
DR N-PSDB; V03230.
XX
PT Hexameric fusion protein containing IgA antibody fragment - used for
PT stimulating CD28 positive cells, or suppressing CTLA-4 positive
PT cells
XX
PS Example 1; Fig 5A-B; 105pp; English.
XX
CC This protein comprises the signal region and extracellular
CC domain of human CD86 encoded by a portion (see V03230) of
CC plasmid CD86fcalphaaplknk. This plasmid encodes a fusion protein
CC comprising the CD86 signal peptide and extracellular domain
CC grafted to a human IgG1 heavy chain FC region and the tailpiece
CC region (alpha-tp) (see W42344) of human IgA heavy chain. The
CC processed fusion protein has been expressed as a hexamer in COS
CC cells. The invention relates to novel hexameric fusion proteins
CC comprising a dimeric binding protein such as CD86 provided at its
CC C-terminus with a tailpiece that has the activity of alpha-tp. The

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CC tailpiece provides the fusion protein with the ability to form
CC stable hexamers. Also claimed are polynucleotides encoding the
CC hexameric fusion proteins, vectors, recombinant host cells and a
CC method for producing the hexamers. The fusion protein is useful in
CC therapeutics and vaccines, and is particularly well suited for
CC applications for which the binding protein from which it is derived
CC is unsatisfactory because of low binding affinity or for
CC applications where multivalency is desired. Applications include
CC diagnostics, binding assays and screening assays. CD86-Ig-alpha-tp
CC fusion protein is used in claimed methods for stimulating CD28
CC positive cells or suppressing CTLA-4 positive cells.
XX
SQ Sequence 260 AA:
QY 1 MDPQCTMGISNLIIFVMAFLISGAAPLKIAVFRNRTADLPCQFRANSQNSISELYVWQD 60
Db 1 mdpqctmgisnliifvmaflisgaaplkiaayfrnrtadlpqfransqnsiselyvtwq 60
QY 61 ENLVINEVYLGEKEKFPDSVSKXYMGRTSPDSQSWTLRLHNLQIKDKGLYOCIIHKKPTGM 120
Db 61 enlvinevylgkfkfsdvshskymgrtfsdsqswtlrlhnlqldkgllyocilhhkptgm 120
QY 121 IRIHONSELSVLANFSOPEIPIVINSITENVTYINLTGSSIHGYPEPKMSVLLRTKNSTI 180
Db 121 irihonseelsvlanfsopeipivinsitenvtynltgssihgypepkmsvllrtnstl 180
QY 181 EYDGIWQKSDQDWTIELYDVSISLSVSFPDYVSNMTIFCLLETDKTRLISPPSTLEDPQ 240
Db 181 eydgiwqksqdwtelydvsislsvsfpdyvsnmtifclletdktrllsspfslsleddp 240
QY 241 PPPDHP 247
Db 241 pppdhp 247

RESULT 7
W86005
ID W86005 standard; Protein; 246 AA.
XX
AC W86005;
XX
DT 15-MAR-1999 (first entry)
DE Human B7-2 extracellular domain and linker.
XX
KW Tumour interacting protein; cancer; gene therapy; vector;
KW 574 antigen; monoclonal antibody; single chain antibody;
KW mouse; human; B7-2; co-stimulatory molecule.
XX
OS Chimeric - Homo sapiens.
XX
FH Chimeric - synthetic.
XX
FH Key
FT Peptide
FT Protein
FT Peptide
XX
PN W09855607-A2.
XX
PD 10-DEC-1998.
XX
PE 04-JUN-1998; 98WO-GB01627.
XX
PR 04-JUL-1997; 97GB-0014230.

```

PR 04-JUN-1997: 97GB-0011579.
PR 20-JUN-1997: 97GB-0013150.
XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX Babbington CR, Carroll MW, Ellard FM, Kingsman SM;
PI Myers KA;
XX
XX WPI; 1999-059910/05.
DR N-PSDB; V80293.
XX
XX New vector encoding a tumour interacting protein for treating cancer
PT - contains a desired nucleotide sequence and/or protein which
PT recognises tumours, and is used as a gene delivery system to treat
PT cancer
XX
XX Example 5; Fig 4; 82pp; English.
PS
XX This polypeptide comprises the extracellular domain (amino acids
CC 1-215) of human co-stimulatory molecule B7-2 joined to a C-terminal
CC flexible peptide linker. It is part of B7-2.5T4.1 co-stimulatory
CC domain, a fusion protein comprising the B7-2 extracellular domain
CC joined via the linker to an scfv (see W86002) derived from murine
CC 5T4 monoclonal antibody. B7-2.5T4.1 cDNA (see V80293) can be
CC inserted into vector pCI to allow expression of the fusion protein
CC in mammalian cells. The trophoblast cell surface antigen defined
CC by 5T4 is expressed at high levels on the cells of a wide variety
CC of human tumours. The invention relates to a vector comprising a
CC nucleotide sequence coding for a tumour interacting protein (TIP)
CC and optionally a nucleotide sequence of interest (NOI) which
CC encodes a protein of interest (POI), the vector being capable of
CC delivering the NOI and/or POI to the tumour recognised by the TIP.
CC Delivery can be in vivo or ex vivo. The vector is used to treat
CC cancer, and may also be used as a gene delivery system for
CC introducing at least 1 gene encoding a TIP (preferably a tumour
CC binding protein) into a haematopoietic cell lineage. B7-2 is
CC expected to bind specifically to CD28 and CTLA-4 present on human
CC T-cells.
XX
XX Sequence 246 AA:

Query Match 72.2%; Score 1252; DB 20; Length 246;
Best Local Similarity 100.0%; Pred. No. 3.8e-107;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 MGLSNILFVMAFLISGAAPLKIQAYFNETADLPQOFANSQNSQISELVVFWODQENLVN 66
DB 1 mglsnllfvmalfllsgaaplkigayfnetadlpqofansqnsiselyvfwgdqenlvln 60
QY 67 EYVIGKEKEFDSVHVKYMRSTFSDSDSWTLRLHNIQIKKGLYOCIIHKKRTGMIRIQM 126
DB 61 evyigkekfdsvhskymgrtsfidsdswclrlhniqikkglyqcllhhkkpctgmrlrhqm 120
QY 127 NSELVLANFSQPEIVPISNTENYINLTCSSIHGYPEPKKMSVLLTRKSTTEYDQIM 186
DB 121 nselvlianfsqpeivpnsntenyinlntcssihgypepkmsvlltrkstleydgm 180
QY 187 OKSODNTELYDVSISLSVSPDYTSNMFTFCILETDKTRLLSPFSTLEDDPQPPDHI 246
DB 181 qksqdnvteilydvsislsvsfpdytsnmftfciletdktrllspfisleddppppdhi 240
QY 247 P 247
DB 241 P 241

RESULT 8
ID W90209 standard; Protein; 244 AA.
XX
AC W90209;
XX

DT 10-MAY-1999 (first entry)
XX
XX hb7.This soluble fusion protein.
DE
XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
KW CD86; T cell activation; inhibitor; graft versus host disease;
KW transplant rejection; allograft rejection; autoimmune disease;
KW allergy; therapy; human; hb7.this.
XX
XX Chimeric - Homo sapiens.
OS Chimeric - synthetic.
XX
XX Key Location/Qualifiers
FH Peptide 1..23
FT /note= "potential eukaryotic secretory signal
FT /note= "peptide"
FT Domain 24..238
FT /note= "human B7.2 (mature protein) extracellular
FT Peptide 239..244
FT /note= "histidine detection/purification tag"

PS Example 3.1.3; Fig 5; 182pp; English.
XX
XX This 28 kDa soluble fusion protein, termed hb7.2hs, is composed
CC of human co-stimulatory molecule B7.2 extracellular domain fused
CC C-terminally to a hexahistidine detection/purification tag. It
CC was produced by PCR amplification (see X01603-04) of hb7.2 cDNA
CC in pCDNAHB7.2 (ICCG2307), insertion of the PCR fragment into
CC baculoviral transfer vector PACS62 and expression in Sf9 Spodoptera
CC as di-bodies, trivalent and tetra-valent antibodies and small
CC antigen binding peptides which can cross-link, or cross-react
CC with, B7.1 and B7.2 expressed on professional antigen presenting
CC cells leading to the inhibition of antigen-specific T cell
CC activation. Methods to produce such molecules are provided. The
CC molecules are used to treat or prevent diseases of the immune
CC system, in particular graft rejection, graft versus host disease,
CC allergy and autoimmune diseases (claimed).
XX
XX Sequence 244 AA:

Query Match 71.6%; Score 1241; DB 20; Length 244;
Best Local Similarity 100.0%; Pred. No. 3.9e-106;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 MGLSNILFVMAFLISGAAPLKIQAYFNETADLPQOFANSQNSQISELVVFWODQENLVN 66
DB 1 mglsnllfvmalfllsgaaplkigayfnetadlpqofansqnsiselyvfwgdqenlvln 60
QY 67 EYVIGKEKEFDSVHVKYMRSTFSDSDSWTLRLHNIQIKKGLYOCIIHKKRTGMIRIQM 126
DB 61 evyigkekfdsvhskymgrtsfidsdswclrlhniqikkglyqcllhhkkpctgmrlrhqm 120
QY 127 NSELVLANFSQPEIVPISNTENYINLTCSSIHGYPEPKKMSVLLTRKSTTEYDQIM 186

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Db      121 nselsvlanfsgpelvpsnltentvynlntcssihgypepkmsvlltrknsleydglm 180
OY      187 OKSDQNTVELYDVSISSVSFPDVTSMNTIFCILETDTKTRLLSPFSIELEDPQPPDH 245
        |||
        181 qksqdnvteiydvsislsfsvfpdvtsmntlfciletdktrllspfsieleddpppph 239

RESULT  9
W90207  standard: protein; 477 AA.
XX
AC      W90207;
XX
DT      10-MAY-1999 (first entry)
XX
DE      hb7.2Fc soluble fusion protein.
XX
KM      B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
KM      CD86; T cell activation; inhibitor; graft versus host disease;
KM      transplant rejection; allograft rejection; autoimmune disease;
KM      allergy; therapy; human; antibody; hb7.1Fc.
XX
OS      Chimeric - Homo sapiens.
OS      Chimeric - synthetic.
XX
FH      Key
FT      Location/Qualifiers
FT      1..16
FT      /note= "potential eukaryotic secretory signal
FT      peptide"
FT      Domain
FT      17..239
FT      /note= "human B7.2 (mature protein) extracellular
FT      Peptide
FT      240..245
FT      /note= "introduced by PCR cloning strategy"
FT      246..477
FT      Protein
FT      /note= "human IgG1-Fc (hinge-CH2-CH3)"
XX
PN      W09858965-A2.
XX
PD      30-DEC-1998.
XX
PF      22-JUN-1998; 98WO-EP03791.
XX
PR      20-JUN-1997; 97EP-0870092.
XX
PA      (INNO-) INNOGENETICS NV.
XX
PI      Bosman A, Buysse M, Lorre K, Sablon E;
PI      WPI; 1999-105615/09.
XX
DR      WPI; 1999-105615/09.
XX
PT      New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PT      immune diseases including allograft rejection
XX
PS      Example 3.1.1.3; Fig 3; 183pp; English.
XX
XX      This 54 kba soluble fusion protein, termed hb7.2Fc, is composed of
XX      human co-stimulatory molecule B7.2 extracellular domain fused
XX      C-terminally to human IgG1-Fc. It was produced by PCR
XX      amplification of hb7.2 cDNA in plasmid pCDNAneo-hb7.2, and
XX      insertion of the amplified cDNA into pVJ-Fc (ICCG3048), resulting
XX      in pVJshb7.2-Fc (ICCG3004) baculotransfer plasmid. The invention
XX      relates to molecules such as diabodies, trivalent and tetravalent
XX      antibodies and small antigen binding peptides which can cross-link,
XX      or cross-react with, B7.1 and B7.2 expressed on professional
XX      antigen presenting cells leading to the inhibition of
XX      antigen-specific T cell activation. Methods to produce such
XX      molecules are provided. The molecules are used to treat or prevent
XX      diseases of the immune system, in particular graft rejection, graft
XX      versus host disease, allergy and autoimmune diseases (claimed).
XX
SQ      Sequence 477 AA;

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```

Query Match      71.6%; Score 1241; DB 20; Length 477;
Best Local Similarity 100.0%; Pred. No. 1e-105;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      7 MGLSNILFVMAFLILSGAAPKIOAYFNETADLPCOFANSONOSLSELYVFWQDQENLYIN 66
        |||
        Db      1 mglsnllfmaflilsgaapklqayfnetadlpcqfansqgselselvvfwqdenlvin 60
OY      67 EYVLGKEKFDPSVHSKYMGRTSPDSWTLRLHNLQIKDKGLYOCIIHHKKPTGMIRIHOM 126
        |||
        Db      61 evylgkekfdpsvhsksyngmrtspdsdswtlrlhnlqikdkglycclihhkkptgmirlhgm 120
OY      127 NSELVLANFSGPELIVISNITENVYINLFCSSIHGYPEPKKMSVLLRTKNSITERYDGM 186
        |||
        Db      121 nselvlianfsgpelivpsnltentvynlntcssihgypepkmsvlltrknsleydglm 180
OY      187 OKSDQNTVELYDVSISSVSFPDVTSMNTIFCILETDTKTRLLSPFSIELEDPQPPDH 245
        |||
        Db      181 qksqdnvteiydvsislsfsvfpdvtsmntlfciletdktrllspfsieleddpppph 239

RESULT  10
Y41076
ID      Y41076 standard: protein; 329 AA.
XX
AC      Y41076;
XX
DT      20-DEC-1999 (first entry)
XX
DE      Canine B7-2 protein.
XX
KM      B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KM      allergic reaction; infectious disease; tumor development; Canine;
KM      graft rejection; inflammation; arthritis; atopic dermatitis.
XX
OS      Canis familiaris.
XX
PN      W09947558-A2.
XX
PD      23-SEP-1999.
XX
PF      19-MAR-1999; 99WO-US06187.
XX
PR      19-MAR-1998; 98US-0078765.
PR      17-APR-1998; 98US-0062597.
XX
PA      (HESK-) HESKA CORP.
XX
PI      Sim G, Yang S, Sellins KS;
PI      WPI; 1999-571822/48.
XX
DR      N-PSDB; 227913, 227915.
XX
PT      New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT      treating, e.g. autoimmune and atopic diseases
XX
PS      Claim 4; Page 97-99; 148pp; English.
XX
XX      The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX      encoding nucleic acid molecules from dogs and cats. The proteins can be
XX      expressed by standard recombinant methodology. The nucleic acid molecules
XX      and the encoded proteins can be used for preventing or treating diseases,
XX      e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX      development, graft rejection, inflammation, arthritic and atopic diseases
XX      such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX      cats, cattle, sheep or pets. The products can also be used for detection,
XX      diagnosis and drug screening.
XX
SQ      Sequence 329 AA;

```

Query Match	57.9%	Score 1003	DB 20	Length 329
Best Local Similarity	62.3%	Pred. No. 4.1e-84		
Matches 205	Conservative 47	Mismatches 71	Indels 6	Gaps 6
QY	4	QCTMGLSILFLVMAFLLSGAPLKLQAYFNFETADLPQFANSOSLSLAVFMWDOENL	63	
Db	4	rcfmetlnmlflfymtlllygaasemkqeyfntkgelphnfhtsnqslsdelvfwgddkl	63	
QY	64	VLINEVYLCKEKFDSYHSKRYMGRTSPDSQSWTLRLNLQIKDKGLYQCIIHHKKPTGMIRI	123	
Db	64	vlyelyrkykqepqvnhrkykgrtsfdkdnwrlrlmlqtkdgllyqctfwhkpxgilypm	123	
QY	124	HQMSNSELVLANFSSQPELIVPISNTEENV-YIMTCSSIHGYEPKMSVLLRTKNTSTY	182	
Db	124	hqmmsdlsvlanfsgpelcmvtsnrtengllnltcsslqgybpexemyflvvtensckky	183	
QY	183	DGIMQSDQNTVELYDVSLISVSFPPDYTSNMTIFCILETDKTRLLSPFSIELE-DPOF	241	
Db	184	dtymksgqnvtelnyvnslsfsfve-asvnslfcvliqlsemkipslypnidantkprp	242	
QY	242	PPDHIPMTITAVL-PLVICVWVFCILMKKKKKRPRRSYKCGTMTMERESQTKRK	300	
Db	243	dgdhlwlaiallmvllvcgmvfiltlrik-ikkkqpshecelnkvkeresegtketr	301	
QY	301	IHIPRSDQAQVREKSSRTSSCDKSDTCE	329	
Db	302	yhetersdeagcv-nlsktasgdnstqf	329	
RESULT 11				
W14944				
ID	W14944	standard; Protein; 250 AA.		
XX				
AC	W14944;			
XX				
DT	16-JUN-1997	(first entry)		
XX				
DE	Chimeric human/porcine CD86.			
XX				
KM	Xenotransplantation; graft rejection; cell interaction; pig;			
XX	CP68; monoclonal antibody; chimeric antibody; diagnosis.			
OS	Chimeric Homo sapiens;			
XX	Chimeric Sus scrofa.			
XX				
FX	Key	Location/Qualifiers		
FT	Peptide	1..25		
FT	Protein	/label= Sig-peptide		
FT	Region	26..250		
FT		/label= Mat_protein		
FT		246..250		
FT		/label= Histidine_tag		
XX				
PN	W09711971-A1.			
XX				
PD	03-APR-1997.			
XX				
PF	27-SEP-1996;	96WO-0515575.		
XX				
PR	26-SEP-1996;	96US-0004489.		
XX				
PR	28-SEP-1995;	95US-0004489.		
XX				
PA	(ALEX-) ALEXION PHARM INC.			
XX				
PI	Eyans MJ, Matis IA, Mueller EE, Mueller JP, Rollins S;			
PI	Rother RP;			
XX				
DR	WPI; 1997-212855/19.			
DR	N-PDB; T62939.			
XX				
PT	Antibodies binding to porcine but not human cell interaction			
PT	proteins - useful to treat and assay for rejection of xenografted			
PT	porcine organs, tissues or cells			

[illegible]

DR WPI: 1999-571822/48.
DR N-PSDB: 227929, 227931.

XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX

PS Claim 4: Page 116-119; 148pp; English.

XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX

SQ Sequence 332 AA:

Query Match 52.6%; Score 912; DB 20; Length 332;

Best Local Similarity 58.4%; Pred. No. 9.3e-76; Mismatches 85; Indels 8; Gaps 7;

Matches 192; Conservative 44; Mismatches 85; Indels 8; Gaps 7;

QY 6 TMGLSNILFVMAFLISGAAPLKIOAYFNETADLPQOFANSQNSISELVFWQDENLVL 65

Db 7 tnglshctllvmalllsgvsmksqayfntgelpchfnsqnsldelvtvfwgqdkl 66

QY 66 NEVYLKKEKFDVSHSKYMGRTSPDSWTLRLNLQIKDKGLYOCIIHKKPTGMIRHQ 125

Db 67 yelfirkepnpvnhlykgrtsfdkdnwclrlhvwqikdgyhchfnykprkylvpmh 126

QY 126 MNSLSVLANFESQPELVPSINTENY-YINLTCSIHGYPEPKKMSVLLRTKNSITFYDG 184

Db 127 msdlsvlanfsgpeltvsnrtensglnlccslygypepkemyfqIntenstkydt 186

QY 185 IMOKSODNTELYDVSISSVSFPDVTSMKTIFFCILETDKTR-LISSPFSIELE--DPOP 241

Db 187 vmkksqnnvtelynvslsfvspe-ahnvsvfcalklletlmlslpIndagpkdkp 245

QY 242 PRDHIPWITAVLEPT-VIICVMVFCILIMKMKKKRPRNSYKCGTMMERESEOTKKRK 300

Db 246 egghfllwlaavlvmfvfvgmwsfkltr-rrkkpqpshcectikretkesqtnerv 304

QY 301 IHIPERDEAQRVFKSKSTSSCDKSDTCF 329

Db 305 yhvperdeagcl-nllktasgdkstnf 332

RESULT 13

Y32285 ID Y32285 standard; Protein; 329 AA.

XX Y32285;

XX 28-FEB-2000 (first entry)

XX Feline CD86 (B7-2).

XX CD86; B7-2; feline; cat; recombinant virus; vaccine;

XX immunomodulator; tumour; cancer; therapy.

XX Fells domesticus.

XX WO957295-A1.

XX 11-NOV-1999.

XX 30-APR-1999; 99WO-US09504.

XX 01-MAY-1998; 98US-0071711.

PA (SCHE) SCHERING-PLOUGH LTD.
PA (SCHE) SCHERING-PLOUGH VETERINARY CORP.

XX Winslow BJ, Cochran MD;

XX WPI: 2000-062155/05.

DR N-PSDB: 234838.

XX Novel recombinant virus useful as immunomodulators, particularly in
PT vaccines

PS Disclosure; Fig 3A; 230pp; English.

XX This sequence represents feline CD86 (B7-2), as deduced from
CC peripheral blood mononuclear cell cDNA (see 234838). Manipulating
CC the expression of CD28 or CTLA-4 (and/or their co-stimulatory
CC ligands CD80 and CD86) regulates T cell proliferation and cytokine
CC release. The invention relates to a recombinant virus that contains
CC at least one foreign nucleic acid, inserted into a nonessential
CC genomic region, that encodes feline CD28, CD80, CD86 or CTLA-4
CC protein, or their immunogenic fragments, and is expressed when the
CC recombinant virus is introduced into a suitable host. The invention
CC also provides: a recombinant virus further comprising a foreign
CC nucleic acid encoding an immunogen derived from a feline pathogen;
CC recombinant viruses capable of enhancing an immune response to
CC protect against disease; recombinant viruses expressing antisense
CC sequences, capable of suppressing an immune response in a feline;
CC e.g. for treatment of autoimmune disease or transplant rejection;
CC and recombinant viruses expressing DNA encoding CD80 and/or CD86
CC used to reduce or eliminate a tumour in cats.

SQ Sequence 329 AA:

Query Match 52.1%; Score 903; DB 21; Length 329;

Best Local Similarity 58.5%; Pred. No. 6.1e-75; Mismatches 83; Indels 8; Gaps 7;

Matches 190; Conservative 44; Mismatches 83; Indels 8; Gaps 7;

QY 6 TMGLSNILFVMAFLISGAAPLKIOAYFNETADLPQOFANSQNSISELVFWQDENLVL 65

Db 7 tnglshctllvmalllsgvsmksqayfntgelpchfnsqnsldelvtvfwgqdkl 66

QY 66 NEVYLKKEKFDVSHSKYMGRTSPDSWTLRLNLQIKDKGLYOCIIHKKPTGMIRHQ 125

Db 67 yelfirkepnpvnhlykgrtsfdkdnwclrlhvwqikdgyhchfnykprkylvpmh 126

QY 126 MNSLSVLANFESQPELVPSINTENY-YINLTCSIHGYPEPKKMSVLLRTKNSITFYDG 184

Db 127 msdlsvlanfsgpeltvsnrtensglnlccslygypepkemyfqIntenstkydt 186

QY 185 IMOKSODNTELYDVSISSVSFPDVTSMKTIFFCILETDKTR-LISSPFSIELE--DPOP 241

Db 187 vmkksqnnvtelynvslsfvspe-ahnvsvfcalklletlmlslpIndagpkdkp 245

QY 242 PRDHIPWITAVLEPT-VIICVMVFCILIMKMKKKRPRNSYKCGTMMERESEOTKKRK 300

Db 246 egghfllwlaavlvmfvfvgmwsfkltr-rrkkpqpshcectikretkesqtnerv 304

QY 301 IHIPERDEAQRVFKSKSTSSCDKS 325

Db 305 yhvperdeagcv-nllktasgdkn 328

RESULT 14

Y32278 ID Y32278 standard; Protein; 329 AA.

XX Y32278;

XX 15-FEB-2000 (first entry)

XX Cat CD86 (B7-2) ligand.

KW CD86: B7-2; ligand; cat; vaccine; feline immunodeficiency virus;
 KW FIV; feline leukemia virus; feline infectious peritonitis virus;
 KW feline panleukopenia virus; feline calicivirus; feline reovirus-3;
 KW feline rotavirus; feline coronavirus; feline syncytial virus;
 KW feline sarcoma virus; feline herpesvirus; feline Borna disease;
 KW rabies virus; Chlamydia; Toxoplasmosis gondii; Dirofilaria immitis;
 KW parasite; autoimmune disease; transplant rejection; therapy.
 XX
 OS Fells domesticus.
 XX
 PN MO9957271-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 30-APR-1999; 99WO-US09502.
 XX
 PR 01-MAY-1998; 98US-0071699.
 XX
 PA (TEXA) TEXAS A & M SYSTEM.
 XX
 PI Collison EW, Hash SM, Choi I;
 XX
 DR WPI: 2000-052972/04.
 DR N-PSDB; 234785.
 XX
 PT Novel feline proteins used to produce feline vaccines which prevent
 PT infectious disease or to promote growth in homologous or heterologous
 PT species -
 XX
 PS Example 1A; Fig 3A; 186pp; English.
 XX
 CC The present sequence represents feline CD86 (B7-2) ligand, as
 CC predicted from isolated cDNA of peripheral blood mononuclear cells.
 CC The coexpression of CD86 with the costimulatory molecules CD28 (see
 CC Y32279) and a tumour antigen or an antigen from a pathogenic
 CC organism has the ability to activate or enhance activation of
 CC T-lymphocytes. Coexpression of CD86 with CTLA-4 (see Y32280) has
 CC the ability to regulate activation of T-lymphocytes. The invention
 CC provides isolated nucleic acids encoding feline CD86 ligand,
 CC feline CD80 (B7-1) ligand, feline CD28 receptor or feline CTLA-4
 CC (CD152) receptor, as well as vectors comprising the nucleic acids,
 CC and polypeptides encoded by the nucleic acids. It also provides
 CC vaccines comprising the CD80, CD86, CD28 or CTLA-4 polypeptides and
 CC further comprising immunogens derived from pathogens, especially
 CC feline immunodeficiency virus (FIV), feline leukemia virus,
 CC feline infectious peritonitis virus, feline panleukopenia virus,
 CC feline calicivirus, feline reovirus-3, feline rotavirus, feline
 CC coronavirus, feline syncytial virus, feline sarcoma virus, feline
 CC herpesvirus, feline Borna disease virus, rabies virus, Chlamydia,
 CC Toxoplasmosis gondii, Dirofilaria immitis, or a flea, bacterial
 CC pathogen, or parasite (all claimed). Vaccines capable of
 CC enhancing an immune response, and vaccines capable of suppressing
 CC an immune response (suitable for treating an autoimmune disease
 CC or tissue or organ transplant rejection) are claimed.
 CC
 XX
 SQ Sequence 329 AA;
 Query Match 52.1%; Score 903; DB 21; Length 329;
 Best Local Similarity 58.5%; Pred. No. 6.1e-75;
 Matches 190; Conservative 44; Mismatches 83; Indels 8; Gaps 7;
 Oy 6 TMGSLNIFVNAFLTSGAFLKIOAYFNEADLPPOFANSONSLSELYVFMODQENL 65
 Db 7 tmgslhllwmlallsvssmksqayfnkgepchtfnsgnsldeylvfwgddqkyl 66
 Oy 66 NEVYLGKEKEDSVHSKYMGRTSPDSWTLRLNHLQIKDKGLYQCIHHKPKPTGIRIQ 125
 Db 67 yelfrfgkqpnvnlkkygtsfdkdwltlrlnhvqkdkgyhcfihykpgkylpmbq 126
 Oy 126 MNSFLVLANSGOPEYPIISITFENV-YINLTGSSIHGVEPEPKMSVLLRTKSTIEYRG 184
 Db 127 msdlsylvlanstgpeitvtsrtfengslndltcsslqgyepkemyfqintnstkydt 186

Oy 185 IMKSDQNTWELDYDVSISVSFSDTSMNTIFCLIEDTKR-LLSPFSIELE--DPQP 241
 Db 187 vmksgnvnlelyvstslpfsyve-ahnvsvfcalikletlmlslpfnldaqpkdqp 245
 Oy 242 PPDHIIPIITFVLEPT-VICVMVFCILIMRKKRRPRNSYKCGTMTRESEOTKKREK 300
 Db 246 eqghflwlaavlvwvfvcgmsfklrk-rlkkkpgpshecelikretkesqcynevp 304
 Oy 301 IHIPERSDAORPKSKTSKTSCKS 325
 Db 305 yhvperdeaqcv-nllktasgdn 328
 RESULT 15
 Y41078
 ID Y41078 standard; protein; 280 AA.
 XX
 AC Y41078;
 XX
 DT 20-DEC-1999 (first entry)
 XX
 DE Canine B7-2s protein.
 XX
 KW B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
 KW allergic reaction; infectious disease; tumor development; canine;
 KW graft rejection; inflammation; arthritis; atopic dermatitis.
 XX
 OS Canis familiaris.
 XX
 PN WO9947558-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 19-MAR-1999; 99WO-US06187.
 XX
 PR 19-MAR-1998; 98US-0078765.
 PR 17-APR-1998; 98US-0062597.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PT Slim G, Yang S, Sellins KS;
 DR WPI: 1999-571822/48.
 DR N-PSDB; 227921, 227923.
 XX
 PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
 PT treating, e.g. autoimmune and atopic diseases
 XX
 PS Claim 4; Page 109-111; 148pp; English.
 XX
 CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC and the encoded proteins can be used for preventing or treating diseases,
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
 CC development, graft rejection, inflammation, arthritis and atopic diseases
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
 CC cats, cattle, sheep or pets. The products can also be used for detection,
 CC diagnosis and drug screening.
 CC
 XX
 SQ Sequence 280 AA;
 Query Match 51.2%; Score 886.5; DB 20; Length 280;
 Best Local Similarity 55.7%; Pred. No. 1.6e-73;
 Matches 182; Conservative 40; Mismatches 54; Indels 51; Gaps 4;
 Oy 4 OCTGSLNIFVNAFLTSGAFLKIOAYFNEADLPPOFANSONSLSELYVFMODQENL 63
 Db 4 rctnelnllfwmlllygaasmksqayfnkgepchtfnsgnsldeylvfwgddqkyl 63
 Oy 64 VLNVEYLGKEKEDSVHSKYMGRTSPDSWTLRLNHLQIKDKGLYQCIHHKPKPTGIRI 123

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Db      64  vlyelyrgkenpqnvhkykgrtsfdkdnwltlhnigdkgfygcfvnhkgpkglvpm 123
QY      124  HQMNSLSTLANFSQPEIYIPISNITEN-YNITCSSHGYPEPKKMSVLLRTKNSTIEY 182
Db      124  hqmsdlsvlanfsgpeimvtsnrtensglinltcssigypepkemyflvktensstky 183
QY      183  DGIOMKSONNVELYDVSISLSVSPDYTSNMTIFCILETDKTRLSSPFSIELEDPQPP 242
Db      184  dvmkxsgnvelnyvnsislsfsype-asnvsifcvlglesmklpslpynie----- 235
QY      243  PDHIPWITAVLPVLIQVWFCLILWKMKKKRPRNSYKCGTNTMERRESEOTKKREKI 302
Db      236  -----tnkverkesegltkeirvyn 254
QY      303  IPERSDPAQRFKSSKTSCTSDKSDTCF 329
Db      255  etersdaqcv-nisklasgdnstqf 280

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